

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 10, 2005, 18:26:54 ; Search time 167 Seconds
(without alignments)

592.878 Million cell updates/sec

Title: US-09-785-019b-335

Perfect score: 1444

Sequence: 1 MQHHHHHSGVDRLNALLP.....TSOLECMTWNQNLGATLKG 256

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1444	100.0	256	5	ABG33384 Human WT1
2	1444	100.0	256	7	ADB67537 Human Wtl
3	1444	100.0	256	7	ADJ80770 Wilm's tu
4	1444	100.0	256	8	ADJ83690 Human WT1
5	1444	100.0	256	8	ADL57578 Human WT-
6	1444	100.0	256	8	ADO09133 Human WT1
7	1418.5	98.2	410	5	ABG33382 Human Trx
8	1418.5	98.2	410	7	ADB67535 Human Trx
9	1418.5	98.2	410	7	ADJ80768 Wilm's tu
10	1418.5	98.2	410	8	ADJ83688 Human WT1
11	1418.5	98.2	410	8	ADL57576 Human Trx
12	1418.5	98.2	410	8	ADO09131 Human Trx
13	1418	98.2	591	5	ABG33383 Human Trx
14	1418	98.2	591	7	ADB67536 Human WT1
15	1418	98.2	591	7	ADJ80769 Wilm's tu
16	1418	98.2	591	8	ADJ83689 Human Trx
17	1418	98.2	591	8	ADL57577 Human Trx
18	1418	98.2	591	8	ADO09132 Human Trx
19	1394	96.5	292	7	ADJ80934 Wilm's tu
20	1394	96.5	292	7	ADJ80905 Wilm's tu
21	1394	96.5	292	8	ADL57713 Human TAT
22	1394	96.5	292	8	ADL57742 Human TAT
23	1394	96.5	292	8	ADO09268 pStumpy-W
24	1394	96.5	292	8	ADO09297 pStumpy-W
25	1394	96.5	321	7	ADJ80914 Wilm's tu

26	1394	96.5	321	7	ADJ80890	Adj80890 Wilm's tu
27	1394	96.5	321	8	ADJ83810	Adj83810 Human Wtl
28	1394	96.5	321	8	ADL57698	Adl57698 Human Wtl
29	1394	96.5	321	8	ADL57722	Adl57722 Human TAT
30	1394	96.5	321	8	ADO09253	Ado09253 Human Wtl
31	1394	96.5	321	8	ADO09277	Ado09277 Codon opt
32	1394	96.5	469	7	ADJ80889	Adj80889 Wilm's tu
33	1394	96.5	469	8	ADJ83809	Adj83809 Human Wtl
34	1394	96.5	469	8	ADL57697	Adl57697 Human Wtl
35	1394	96.5	469	8	ADO09252	Ado09252 Human Wtl
36	1386	96.0	280	7	ADJ80896	Adj80896 Wilm's tu
37	1386	96.0	280	8	ADJ83816	Adj83816 Human Wtl
38	1386	96.0	280	8	ADL57704	Adl57704 Human Wtl
39	1386	96.0	280	8	ADO09259	Ado09259 Human Wtl
40	1386	96.0	281	7	ADJ80900	Adj80900 Wilm's tu
41	1386	96.0	281	8	ADJ83820	Adj83820 Recombina
42	1386	96.0	281	8	ADL57708	Adl57708 Human Wtl
43	1386	96.0	281	8	ADO09263	Ado09263 Human Wtl
44	1386	96.0	291	7	ADJ80899	Adj80899 Wilm's tu
45	1386	96.0	291	8	ADJ83819	Adj83819 Recombina

ALIGNMENTS

RESULT 1

ABG33384

ID ABG33384 standard; protein; 256 AA.

XX AC ABG33384;

XX DT 15-JUL-2002 (first entry)

XX DE Human Wtl-A.

XX KW Human; mouse; cytostatic; immunostimulant; Wtl; cancer; immune response.

XX OS Homo sapiens.

XX PN WO200228414-A1.

XX PD 11-APR-2002.

XX PF 03-OCT-2001; 2001WO-US031139.

XX PR 06-OCT-2000; 2000US-00684361.

XX PR 09-OCT-2000; 2000US-00685830.

XX PR 15-FEB-2001; 2001US-00785019.

XX PR 24-AUG-2001; 2001US-00938864.

(CORI-) CORIXA CORP.

(GAIG/) GAIGER A.

PI Gaiger A, McNeill PD, Smithgall M, Moulton G, Vedvick TS;

PI Sleath PR, Mossman S, Evans L, Spies AG, Boydston J;

DR WPI; 2002-352217/38.

XX N-PSDB; ABK69666.

PT Novel isolated Wtl polynucleotide, and encoded polypeptide, useful for

PT treating and diagnosing cancer in a patient.

PS Claim 2; Page 223-224; 260pp; English.

CC The invention relates to an isolated Wtl polynucleotide (I) and

CC polypeptide encoded by (I). The Wtl polynucleotides and polypeptides are

CC used for treating and detecting cancer in a patient, and for stimulating

CC an immune response in patient. ABG33070-ABG33405 represent Wtl amino acid

CC sequences of the invention

XX Sequence 256 AA;

SQ Query Match 100.0%; Score 1444; DB 5; Length 256;

Best Local Similarity 100.0%; Pred. No. 2.2e-104;		Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 MQHHHHGSDVRLNALLPAVPSLGGGGGCGALPVSGAAQWAPVLDFAFPASAYSLGG 60		
Db	1 MQHHHHGSDVRLNALLPAVPSLGGGGGCGALPVSGAAQWAPVLDFAFPASAYSLGG 60		
QY	61 PAPPAPPPPPPPPHSFIKQEPSWGAEPHEQCISAFVHESGQFTGTAGACRYGPG 120		
Db	61 PAPPAPPPPPPPPHSFIKQEPSWGAEPHEQCISAFVHESGQFTGTAGACRYGPG 120		
QY	121 PPPPSQASSQARMFPNAPVLPSCLESQPAIRNQGYSTVTFDGTSPSYGHTPSSHAAQFPN 180		
Db	121 PPPPSQASSQARMFPNAPVLPSCLESQPAIRNQGYSTVTFDGTSPSYGHTPSSHAAQFPN 180		
QY	181 HSFKHEDPMQGGSLGEGQQYVPPVYVGGCHTPTDCTGSOALLRTPYSSDNLQYMTSQL 240		
Db	181 HSFKHEDPMQGGSLGEGQQYVPPVYVGGCHTPTDCTGSOALLRTPYSSDNLQYMTSQL 240		
QY	241 ECMTWQNMNLGATLKG 256		
Db	241 ECMTWQNMNLGATLKG 256		
RESULT 2			
AD867537	AD867537 standard; protein; 256 AA.		
XX	AC	ADB67537;	
XX	DT	04-DEC-2003 (first entry)	
XX	DE	Human Wilm's tumour protein, WT1A.	
XX	KW	Human; Wilm's tumour antigen; WT1; cytostatic; antigen; T cell;	
XX	KW	antigen-presenting cell; CD4+; CD8+; immune response; cancer; vaccine;	
XX	KW	leukaemia; antigen.	
XX	OS	Homo sapiens.	
XX	PN	US2003072767-A1.	
XX	PD	17-APR-2003.	
XX	PF	24-AUG-2001; 2001US-00938864.	
XX	PR	30-SEP-1998; 98US-00164223.	
XX	PR	25-MAR-1999; 99US-00276484.	
XX	PR	06-OCT-2000; 2000US-00684361.	
XX	PR	09-OCT-2000; 2000US-00685830.	
XX	PR	15-FEB-2001; 2001US-00785019.	
XX	PA	(GAIG/) GAIGER A.	
XX	PA	(MCNE/) MCNEILL P D.	
XX	PA	(SMIT/) SMITHGALL M.	
XX	PA	(MOUL/) MOULTON G.	
XX	PA	(VEDV/) VEDVICK T S.	
XX	PA	(SLEA/) SLEATH P R.	
XX	PA	(MOSS/) MOSSMAN S.	
XX	PA	(EVAN/) EVANS L.	
XX	PA	(SPIE/) SPIES A G.	
XX	PA	(BOYD/) BOYDSTON J.	
XX	PI	Gaiger A, Mcneill PD, Smithgall M, Moulton G, Vedvick TS;	
XX	PI	Sleath PR, Mosseman S, Evans L, Spies AG, Boydston J;	
XX	DR	WPI; 2003-605957/57.	
XX	DR	N-PSDB; ADB67532.	
XX	PT	Novel Wilms tumor polynucleotides encoding WT1 polypeptides, useful for	
XX	PT	detecting the presence of cancer in a patient, and in pharmaceutical	
XX	PT	compositions, e.g. vaccines, for treating cancers e.g. leukemia.	

PS	Claim 2; Page 127; 197pp; English.		
XX	The invention relates to an isolated Wilm tumour (WT1) polynucleotide		
CC	comprising a full length protein, truncated protein, mutated protein or		
CC	fusion protein. Also included are the encoded WT1 proteins, expression		
CC	vectors, host cells, antibodies, detecting the presence of a cancer in a		
CC	patient by contacting a biological sample with a binding agent that binds		
CC	to a WT1 protein, an oligonucleotide that hybridises to a WT1		
CC	polynucleotide, stimulating and/or expanding T cells specific for a		
CC	tumour protein by contacting T cells with the WT1 polynucleotide, the WT1		
CC	protein or antigen-presenting cells that express the WT1 protein, a		
CC	composition (C1) comprising physiologically acceptable carriers and		
CC	immunostimulants as first component, and a second component selected from		
CC	the WT1 polynucleotide, the WT1 protein, Ab, or T cells and antigen		
CC	presenting cells that express the WT1 protein, inhibiting the		
CC	development of a cancer in a patient (by incubating CD4+ and/or CD8+ T		
CC	cells isolated from a patient with the WT1 polynucleotide, the WT1		
CC	protein or antigen presenting cells that express the WT1 protein, such		
CC	that T cell proliferate, administering the proliferated T cells to the		
CC	patient, and thus inhibiting the development of a cancer in the patient)		
CC	and a composition (C2) comprising a WT1 polypeptide resuspended in a		
CC	buffer comprising at least 1-3 sugars selected from trehalose, maltose,		
CC	sucrose, fructose and glucose, at a concentration of 7-13% and		
CC	optionally ethanolamine, cysteine and polysorbate-80, or WT1 polypeptide		
CC	and MPL-SE or Enhanzyn). Also disclosed as anew are polypeptides		
CC	comprising a variant of an immunogenic portion of WT1 polypeptide. C1 is		
CC	useful for stimulating immune response in a patient, and for treating		
CC	cancer in a patient. The oligonucleotide is also useful for determining		
CC	the presence of a cancer in a patient. The WT1 polynucleotide and the WT1		
CC	protein are useful in pharmaceutical compositions, e.g. vaccines, the WT1		
CC	protein is useful as marker to indicate the presence or absence of a		
CC	cancer. C1 is useful for inhibiting the development of a malignant		
CC	disease in a patient, for preventing and treating metastatic diseases		
CC	e.g. leukaemia and cancer, and for removing tumour cells from a		
CC	biological sample. Ab (binding agent for the WT1 protein) is useful for		
CC	detecting the presence of cancer in a patient. The present sequence is		
XX	the Human Wilm's tumour gene product, WT1 protein.		
SQ	Sequence 256 AA;		
Query Match		100.0%;	Score 1444; DB 7; Length 256;
Best Local Similarity		100.0%;	Pred. No. 2.2e-104;
Matches 256;		Conservative 0;	Mismatches 0; Indels 0; Gaps 0;
QY	1 MQHHHHGSDVRLNALLPAVPSLGGGGGCGALPVSGAAQWAPVLDFAFPASAYSLGG 60		
Db	1 MQHHHHGSDVRLNALLPAVPSLGGGGGCGALPVSGAAQWAPVLDFAFPASAYSLGG 60		
QY	61 PAPPAPPPPPPPPHSFIKQEPSWGAEPHEQCISAFVHESGQFTGTAGACRYGPG 120		
Db	61 PAPPAPPPPPPPPHSFIKQEPSWGAEPHEQCISAFVHESGQFTGTAGACRYGPG 120		
QY	121 PPPPSQASSQARMFPNAPVLPSCLESQPAIRNQGYSTVTFDGTSPSYGHTPSSHAAQFPN 180		
Db	121 PPPPSQASSQARMFPNAPVLPSCLESQPAIRNQGYSTVTFDGTSPSYGHTPSSHAAQFPN 180		
QY	181 HSFKHEDPMQGGSLGEGQQYVPPVYVGGCHTPTDCTGSOALLRTPYSSDNLQYMTSQL 240		
Db	181 HSFKHEDPMQGGSLGEGQQYVPPVYVGGCHTPTDCTGSOALLRTPYSSDNLQYMTSQL 240		
QY	241 ECMTWQNMNLGATLKG 256		
Db	241 ECMTWQNMNLGATLKG 256		
RESULT 3			
ADJ80770	ADJ80770 standard; protein; 256 AA.		
XX	AC	ADJ80770;	
XX	AC	ADJ80770;	
XX	DT	06-MAY-2004 (first entry)	

DE Wilm's tumor antigen associated protein #4.
XX cytostatic; gene therapy; vaccine; Wilm's tumor antigen; Wt1; cancer;
KW leukemia.
XX Homo sapiens.
OS WO2003037060-A2.
XX 08-MAY-2003.
XX 30-OCT-2002; 2002WO-US035194.
XX 30-OCT-2001; 2001US-00002603.
PR 16-APR-2002; 2002US-00125635.
PR 12-JUL-2002; 2002US-00195835.
PR 16-SEP-2002; 2002US-00244830.
XX (CORI-) CORIXA CORP.
PA (GAIG/) GAIGER A.
XX Gaiger A, McNeill PD, Jaya N, Carter D;
XX WPI; 2003-430453/40.
XX New isolated polypeptide for diagnosing, preventing or treating malignant
PT diseases, e.g. cancer or leukemia, comprises an immunogenic portion of a
PT Wilm's tumor antigen.
XX Disclosure; SEQ ID NO 335; 371pp; English.
XX The invention relates to an isolated polypeptide comprising an
CC immunogenic portion of a Wilm's tumor antigen, or its variant that
CC differs in one or more substitutions, deletions, additions and/or
CC insertions, such that the ability of the variant to react with Wt1-
CC specific antisera and/or T-cell lines or clones is not substantially
CC diminished. The composition and methods are useful in diagnosing,
CC preventing or treating malignant diseases, such as cancer or leukemia.
CC This sequence represents a protein of the invention.
XX Sequence 256 AA;
XX
Query Match 100.0%; Score 1444; DB 7; Length 256;
Best Local Similarity 100.0%; Pred. No. 2.2e-104;
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQHHHHHSGSDVRDLNALLPAVPSLGGGGGCGALPVSGAAQWAPVLDPAFPASAYSLGG 60
DB 1 MQHHHHHSGSDVRDLNALLPAVPSLGGGGGCGALPVSGAAQWAPVLDPAFPASAYSLGG 60
QY 61 PAPPAPPPPPPPPHSFIKQEPSWGGAEPHEQCLSAFTVHFGSQTGTAGACRYGPF 120
DB 61 PAPPAPPPPPPPPHSFIKQEPSWGGAEPHEQCLSAFTVHFGSQTGTAGACRYGPF 120
QY 121 PPPPSOASSGOARMFNAPVLPSCLESQPAIRNQGYSTVTFDGTGTSQALLLRTPTSSDNLQYMTSQL 180
DB 121 HSPKHEPDMGQSGSLGEEQYVSPVPVYCHTPTDCTGSOALLLRTPTSSDNLQYMTSQL 240
QY 181 HSPKHEPDMGQSGSLGEEQYVSPVPVYCHTPTDCTGSOALLLRTPTSSDNLQYMTSQL 240
DB 181 HSPKHEPDMGQSGSLGEEQYVSPVPVYCHTPTDCTGSOALLLRTPTSSDNLQYMTSQL 240
QY 241 ECMTWNQMLGATLKG 256
DB 241 ECMTWNQMLGATLKG 256
RESULT 4
ID ADJ83690
XX ADJ83690 standard; protein; 256 AA.
AC ADJ83690;
XX

DT 06-MAY-2004 (first entry)
XX Human Wt1 (Wilm's tumour)-related Wt1_A protein.
XX Immune response; Wt1; Wilm's tumour; immunostimulant; cytostatic; vaccine;
KW malignant disease; leukaemia; cancer; human; Wt1_A.
XX Homo sapiens.
OS US2003235557-A1.
XX 25-DEC-2003.
XX 16-SEP-2002; 2002US-00244830.
XX 30-SEP-1998; 98US-00164223.
PR 25-MAR-1999; 99US-00276484.
PR 06-OCT-2000; 2000US-00684361.
PR 09-OCT-2000; 2000US-00685830.
PR 15-FEB-2001; 2001US-00785019.
PR 24-AUG-2001; 2001US-00938864.
PR 30-OCT-2001; 2001US-00002603.
PR 16-APR-2002; 2002US-00125635.
PR 12-JUL-2002; 2002US-00195835.
XX (CORI-) CORIXA CORP.
PA Gaiger A, Cheever MA;
XX WPI; 2004-070542/07.
XX N-PSDB; ADJ83685.
XX Inducing an immune response in an animal, useful for treating or
PT preventing cancer, comprises administering a composition comprising a
PT viral vector comprising an immunogenic portion of a Wt1 polynucleotide.
XX Example 9; SEQ ID NO 335; 229pp; English.
XX The invention relates to a novel method for inducing an immune response
CC in an animal which involves administering a first and a second
CC composition comprising a first and a second viral vector, respectively,
CC each having at least an immunogenic portion of a Wt1 (Wilm's tumour)
CC polynucleotide operably linked to an expression control sequence. The
CC method of the invention has immunostimulant and cytostatic applications
CC and may be useful for generating or enhancing an immune response to Wt1,
CC possibly via the production of a vaccine, as well as for preventing
CC and/or treating malignant diseases such as leukaemia and cancer. The
CC current sequence is that of the human Wt1-related protein of the
CC invention.
XX Sequence 256 AA;
XX
Query Match 100.0%; Score 1444; DB 8; Length 256;
Best Local Similarity 100.0%; Pred. No. 2.2e-104;
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQHHHHHSGSDVRDLNALLPAVPSLGGGGGCGALPVSGAAQWAPVLDPAFPASAYSLGG 60
DB 1 MQHHHHHSGSDVRDLNALLPAVPSLGGGGGCGALPVSGAAQWAPVLDPAFPASAYSLGG 60
QY 61 PAPPAPPPPPPPPHSFIKQEPSWGGAEPHEQCLSAFTVHFGSQTGTAGACRYGPF 120
DB 61 PAPPAPPPPPPPPHSFIKQEPSWGGAEPHEQCLSAFTVHFGSQTGTAGACRYGPF 120
QY 121 PPPPSOASSGOARMFNAPVLPSCLESQPAIRNQGYSTVTFDGTGTSQALLLRTPTSSDNLQYMTSQL 180
DB 121 HSPKHEPDMGQSGSLGEEQYVSPVPVYCHTPTDCTGSOALLLRTPTSSDNLQYMTSQL 240
QY 181 HSPKHEPDMGQSGSLGEEQYVSPVPVYCHTPTDCTGSOALLLRTPTSSDNLQYMTSQL 240
DB 181 HSPKHEPDMGQSGSLGEEQYVSPVPVYCHTPTDCTGSOALLLRTPTSSDNLQYMTSQL 240
QY 241 ECMTWNQMLGATLKG 256

Db	241	ECMTWNQNMIGATLKG	256
RESULT 5			
ADL57578			
ID	ADL57578	standard; protein; 256 AA.	
AC	ADL57578;		
XX			
DT	20-MAY-2004	(first entry)	
XX			
DE	Human WT-1 N-terminal open reading frame, WT-1A.		
XX			
KW	Human; Wilms' tumour; WT1; cancer; cytostatic; immunogen; antigen; vaccine; T-cell; MHC; Major Histocompatibility Complex; HLA-A2;		
KW	human leukocyte antigen; Ral2; HIS tag; twin arginine translocator; TAT;		
KW	malignant disease; mutein; mutant.		
XX			
OS	Homo sapiens.		
OS	Synthetic.		
XX			
PN	US2003215458-A1.		
XX			
PD	20-NOV-2003.		
XX			
PF	30-OCT-2002; 2002US-00286333.		
XX			
PR	30-SEP-1998; 98US-00164223.		
XX			
PR	25-MAR-1999; 99US-00276484.		
PR	06-OCT-2000; 2000US-00684361.		
PR	09-OCT-2000; 2000US-00685830.		
PR	15-FEB-2001; 2001US-00785019.		
PR	24-AUG-2001; 2001US-00938864.		
PR	30-OCT-2001; 2001US-00002603.		
PR	16-APR-2002; 2002US-00125635.		
PR	12-JUL-2002; 2002US-00195835.		
PR	16-SEP-2002; 2002US-00244830.		
XX			
FA	(CORI-) CORIXA CORP.		
XX			
PI	Gaiger A, Mcneill PD, Jaya N;		
XX			
XX	WPI; 2004-021827/02.		
DR	N-FSDB; ADL57573.		
XX			
PT	New polypeptides and polynucleotides useful for generating or enhancing		
PT	an immune response to Wilms' tumor, or for treating and/or preventing		
PT	malignant diseases, e.g. cancer.		
XX			
PS	Example 9; SEQ ID NO 335; 259pp; English.		
XX			
CC	The invention relates to an isolated polypeptide comprising an		
CC	immunogenic portion of a Wilms' tumour antigen (WT1), or their variants		
CC	that differs in substitution(s), deletion(s), addition(s) and/or		
CC	insertion(s), where ability of the variant to react with WT1-specific		
CC	antisera and/or T-cell lines or clones is not substantially diminished.		
CC	Also included are a fusion protein comprising at least one WT1		
CC	polypeptide, an isolated polynucleotide encoding the fusion protein, a		
CC	composition comprising a WT1 polypeptide in combination with a		
CC	pharmaceutical carrier or excipient, a vaccine comprising a WT1		
CC	polypeptide in combination with a non-specific immune response enhancer,		
CC	an expression vector comprising the polynucleotide operably linked to an		
CC	expression control sequence and a host cell transformed or transfected		
CC	with the expression vector. The immunogenic portion of the WT1		
CC	polypeptide has been modified such that the ability of the immunogenic		
CC	portion to bind to an MHC (Major Histocompatibility Complex) molecule or		
CC	to HLA-A2 is increased relative to that of the immunogenic portion. The		
CC	WT1 polypeptide may comprise a Wilms' tumour antigen having a deletion of		
CC	a proline rich region at amino acid positions 54-68 of the Wilms' tumour		
CC	antigen. The fusion partner is selected from Ral2, protein D, LYTA, a HIS		
CC	tag, a targeting signal capable of directing a polypeptide to the		
CC	endosomal/lysosomal compartment, twin arginine translocator (TAT), and		
CC			
CC	truncated twin arginine translocator. The polypeptide, polynucleotide or		
CC	compositions comprising them may be used for generating or enhancing an		
CC	immune response to Wilms' tumour, and for treating and/or preventing		
CC	malignant diseases, e.g. cancer. The compositions may be used as markers		
CC	for the progression of cancer. The present sequence is a mutated or		
CC	truncated WT-1 protein.		
XX			
SQ	Sequence 256 AA;		
	Query Match 100.0%; Score 1444; DB 8; Length 256;		
	Best Local Similarity 100.0%; Pred. No. 2.2e-104; Indels 0; Gaps 0;		
	Matches 256; Conservative 0; Mismatches 0;		
QY	1	MQHHHHHSGSDVRLDNLNALLPAVPSLGGGGGCGALPVSGAAQWAPVLDFAAPPASAYGSLGG	60
Db	1	MQHHHHHSGSDVRLDNLNALLPAVPSLGGGGGCGALPVSGAAQWAPVLDFAAPPASAYGSLGG	60
QY	61	PAPPPAPPPPPPPPHSFYKQPSWGGABPHEEQCLSAFTVHFSGQFTGTAGACRYGPGF	120
Db	61	PAPPPAPPPPPPPPHSFYKQPSWGGABPHEEQCLSAFTVHFSGQFTGTAGACRYGPGF	120
QY	121	PPPSQASSGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTSPYGHTPSHHAAQFPN	180
Db	121	PPPSQASSGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTSPYGHTPSHHAAQFPN	180
QY	181	HGFKHEDPMGQGSGLGEQQYSVPPVYGCHTPTDCTGSOALLLRTPYSSDNLQYMTSQL	240
Db	181	HGFKHEDPMGQGSGLGEQQYSVPPVYGCHTPTDCTGSOALLLRTPYSSDNLQYMTSQL	240
QY	241	ECMTWNQNMIGATLKG	256
Db	241	ECMTWNQNMIGATLKG	256
RESULT 6			
ADL57573			
ID	ADL57573	standard; protein; 256 AA.	
XX			
AC	ADL57573;		
XX			
DT	01-JUL-2004	(first entry)	
XX			
DE	Human WT1_A.		
XX			
KW	Wilms' tumour antigen; WT1; vaccine; malignant disease; immunogenic;		
KW	leukaemia; cancer; human.		
XX			
OS	Homo sapiens.		
XX			
PN	US2004018204-A1.		
XX			
PD	29-JAN-2004.		
XX			
XX	30-APR-2003; 2003US-00427717.		
XX			
PR	24-AUG-2001; 2001US-00938864.		
PR	30-OCT-2001; 2001US-00002603.		
PR	16-APR-2002; 2002US-00125635.		
PR	12-JUL-2002; 2002US-00195835.		
PR	16-SEP-2002; 2002US-00244830.		
PR	30-OCT-2002; 2002US-00286333.		
XX			
PA	(CORI-) CORIXA CORP.		
XX			
PI	Gaiger A, Mcneill PD, Jaya N;		
XX			
XX	WPI; 2004-121992/12.		
DR	N-FSDB; ADL57573.		
XX			
PT	New polypeptides and polynucleotides comprising an immunogenic portion of		
PT	a Wilms' tumor antigen, useful as vaccines for preventing or treating		
PT	malignant diseases, e.g. cancer or leukemia.		
XX			

PS Example 9; SEQ ID NO 335; 252pp; English.

XX The invention relates to an isolated polypeptide which comprises an

CC immunogenic portion of a Wilms' tumour antigen having a deletion of a

CC proline rich region, so that the ability of the variant to react with Wt1

CC -specific antiserum and/or T-cell lines or clones is not substantially

CC diminished. The polypeptide is useful as a vaccine in combination with a

CC non-specific immune response enhancer for preventing malignant diseases.

CC The polypeptide is useful for enhancing or inducing an immune response in

CC a patient; for inhibiting the development of malignant disease in a

CC patient; for stimulating or expanding T cells. The polypeptides,

CC polynucleotides and compositions are useful for treating malignant

CC diseases including leukaemia and cancer. The present sequence represents

CC the amino acid sequence of a human Wt1.

XX SQ Sequence 256 AA;

Query Match 100.0%; Score 1444; DB 8; Length 256;

Best Local Similarity 100.0%; Pred. No. 2.2e-104; Mismatches 0; Indels 0; Gaps 0;

Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQHHHHHSDVRLNALLPAVPSLGGGGCALPVSGAAQWAPVLDFAFPASAYGSLGG 60

DB 1 MQHHHHHSDVRLNALLPAVPSLGGGGCALPVSGAAQWAPVLDFAFPASAYGSLGG 60

QY 61 PAPPAPPPPPPPHFFIKQEPSWGAEPHEOCLSAFTVHFGQGTGTAGACRYGPF 120

DB 61 PAPPAPPPPPPPHFFIKQEPSWGAEPHEOCLSAFTVHFGQGTGTAGACRYGPF 120

QY 121 PPPPSQASSGOARMPNAPVLPSCLESQAIRNOGYSTVTFDGTSPSYGHTPSHHAAQFPN 180

DB 121 PPPPSQASSGOARMPNAPVLPSCLESQAIRNOGYSTVTFDGTSPSYGHTPSHHAAQFPN 180

QY 181 HSFKHEDPMQOQSLGQQSVPPPVYVGGHTPTDSCSGQALLLRTPYSSDNLQYMTSQL 240

DB 181 HSFKHEDPMQOQSLGQQSVPPPVYVGGHTPTDSCSGQALLLRTPYSSDNLQYMTSQL 240

QY 241 ECMTWNQNLGATLKG 256

DB 241 ECMTWNQNLGATLKG 256

RESULT 7

ABG33382

ID ABG33382 standard; protein; 410 AA.

XX AC ABG33382;

XX DT 15-JUL-2002 (first entry)

XX DE Human Trx_Wt1_A.

XX KW Human; mouse; cytostatic; immunostimulant; Wt1; cancer; immune response.

XX OS Homo sapiens.

XX PN WO200228414-A1.

XX PD 11-APR-2002.

XX PF 03-OCT-2001; 2001WO-US031139.

XX PR 06-OCT-2000; 2000US-00684361.

XX PR 09-OCT-2000; 2000US-00684361.

XX PR 13-FEB-2001; 2001US-00785019.

XX PR 24-AUG-2001; 2001US-00938864.

XX (CORI-) CORIXA CORP.

XX (GAIG/) GAIGER A.

XX PI Gaiger A, McNeill PD, Smithgall M, Moulton G, Vedvick TS;

XX PI Sleath PR, Moseman S, Evans L, Spies AG, Boydston J;

DR WPI; 2002-352217/38.

XX N-PSDB; ABK69664.

PT Novel isolated Wt1 polynucleotide, and encoded polypeptide, useful for

XX treating and diagnosing cancer in a patient.

PS Claim 2; Page 221-222; 260pp; English.

XX The invention relates to an isolated Wt1 polynucleotide (I) and

CC the polypeptide encoded by (I). The Wt1 polynucleotides and polypeptides are

CC used for treating and detecting cancer in a patient, and for stimulating

CC an immune response in patient. ABG33070-ABG33405 represent Wt1 amino acid

CC sequences of the invention

XX SQ Sequence 410 AA;

Query Match 98.2%; Score 1418.5; DB 5; Length 410;

Best Local Similarity 89.2%; Pred. No. 3.5e-102;

Matches 256; Conservative 0; Mismatches 0; Indels 31; Gaps 1;

QY 1 MQHHHHH-----GSDVRDLNALLPAVPSLGGG 29

DB 124 MQHHHHHVSIEGRASSGGLVPRGSSGDDDDKSSRGSDVRDLNALLPAVPSLGGG 183

QY 30 GCALPVSGAAQWAPVLDFAFPASAYGSLGGPAPPAPPPPPHFFIKQEPSWGA 89

DB 184 GCALPVSGAAQWAPVLDFAFPASAYGSLGGPAPPAPPPPPHFFIKQEPSWGA 243

QY 90 PHEOCLSAFTVHFGQGTGTAGACRYGPFPPPSQASSGOARMPNAPVLPSCLESQ 149

DB 244 PHEOCLSAFTVHFGQGTGTAGACRYGPFPPPSQASSGOARMPNAPVLPSCLESQ 303

QY 150 AIRNOGYSTVTFDGTSPSYGHTPSHHAAQFPNHSFKHEDPMQOQSLGQQSVPPPVYGC 209

DB 304 AIRNOGYSTVTFDGTSPSYGHTPSHHAAQFPNHSFKHEDPMQOQSLGQQSVPPPVYGC 363

QY 210 HTPTDSCSGQALLLRTPYSSDNLQYMTSQLQECMTWNQNLGATLKG 256

DB 364 HTPTDSCSGQALLLRTPYSSDNLQYMTSQLQECMTWNQNLGATLKG 410

RESULT 8

ADB67535

ID ADB67535 standard; protein; 410 AA.

XX AC ADB67535;

XX DT 04-DEC-2003 (first entry)

XX DE Human Wt1-A-Trx fusion protein.

XX KW Human; Wilm's tumour antigen; Wt1; cytostatic; antigen; T cell;

XX KW antigen-presenting cell; CD4+; CD8+; immune response; cancer; vaccine;

XX KW leukaemia; antigen.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN US2003072767-A1.

XX PD 17-APR-2003.

XX PF 24-AUG-2001; 2001US-00938864.

XX PR 30-SEP-1998; 98US-00164223.

XX PR 25-MAR-1999; 99US-00276484.

XX PR 06-OCT-2000; 2000US-00684361.

XX PR 09-OCT-2000; 2000US-00684361.

XX PR 15-FEB-2001; 2001US-00785019.

XX (GAIG/) GAIGER A.

XX (MCNE/) MCNEILL P D.

XX (SMIT/) SMITHGALL M.

PA (MOUL/) MOULTON G.
 PA (VEDV/) VEDVICK T. S.
 PA (SLEA/) SLEATH P. R.
 PA (MOSS/) MOSSMAN S.
 PA (EVAN/) EVANS L.
 PA (SPIE/) SPIES A. G.
 PA (BOYD/) BOYDSTON J.
 XX
 PI Gaiger A, McNeill PD, Smithgall M, Moulton G, Vedvick TS;
 PI Sleath PR, Mossman S, Evans L, Spies AG, Boydston J;
 XX
 DR WPI: 2003-605957/57.
 DR N-PSDB; ADB67530.
 XX
 PT Novel Wilm's tumor polynucleotides encoding Wt1 polypeptides, useful for
 PT detecting the presence of cancer in a patient, and in pharmaceutical
 PT compositions, e.g. vaccines, for treating cancers e.g. leukemia.
 XX
 PS Claim 2; Page 124-125; 197pp; English.
 XX
 CC The invention relates to an isolated Wilm's tumor (Wt1) polynucleotide
 CC comprising a full length protein, truncated protein, mutated protein or
 CC fusion protein. Also included are the encoded Wt1 proteins, expression
 CC vectors, host cells, antibodies, detecting the presence of a cancer in a
 CC patient by contacting a biological sample with a binding agent that binds
 CC to a Wt1 protein, an oligonucleotide that hybridizes to a Wt1
 CC polynucleotide, stimulating and/or expanding T cells specific for a
 CC tumour protein by contacting T cells with the Wt1 polynucleotide, the Wt1
 CC protein or antigen-presenting cells that express the Wt1 protein, a
 CC composition (C1) comprising physiologically acceptable carriers and
 CC immunostimulants as first component, and a second component selected from
 CC the Wt1 polynucleotide, the Wt1 protein, Ab, or T cells and antigen
 CC presenting cells that express the Wt1 protein, inhibiting the
 CC development of a cancer in a patient (by incubating CD4+ and/or CD8+ T
 CC cells isolated from a patient with the Wt1 polynucleotide, the Wt1
 CC protein or antigen-presenting cells that express the Wt1 protein, such
 CC that T cell proliferate, administering the proliferated T cells to the
 CC patient, and thus inhibiting the development of a cancer in the patient)
 CC and a composition (C2) comprising a Wt1 polypeptide resuspended in a
 CC buffer comprising at least 1-3 sugars selected from trehalose, maltose,
 CC sucrose, fructose and glucose, at a concentration of 7-13%, and
 CC optionally ethanolamine, cysteine and Polysorbate-80, or Wt1 polypeptide
 CC and MPL-SE or Enhancyn). Also disclosed as new are polypeptides
 CC comprising a variant of an immunogenic portion of Wt1 polypeptide. C1 is
 CC useful for stimulating immune response in a patient, and for treating
 CC cancer in a patient. The oligonucleotide is also useful for determining
 CC the presence of a cancer in a patient. The Wt1 polynucleotide and the Wt1
 CC protein are useful in pharmaceutical compositions, e.g. vaccines. the Wt1
 CC protein is useful as marker to indicate the presence or absence of a
 CC cancer. C1 is useful for inhibiting the development of a malignant
 CC disease in a patient, for preventing and treating metastatic diseases
 CC e.g. leukemia and cancer, and for removing tumour cells from a
 CC biological sample. Ab (binding agent for the Wt1 protein) is useful for
 CC detecting the presence of cancer in a patient. The present sequence
 CC represents a Human Wt1 fusion protein.
 XX
 SQ Sequence 410 AA;
 Query Match 98.2%; Score 1418.5; DB 7; Length 410;
 Best Local Similarity 89.2%; Pred. No. 3.5e-102;
 Matches 256; Conservative 0; Mismatches 0; Indels 31; Gaps 1;
 1 MQHHHHH-----GSDVRDLNALLPAVPSLGGG 29
 124 MQHHHHHVTEGRASSGGGLVPRGSGGDDDDKSSRGSDVRDLNALLPAVPSLGGG 183
 30 GCALPVSGAAQWAPVLDFAFGASAYSLGPGAPPPPPPPPHSFYKQEPSWGAE 89
 184 GCALPVSGAAQWAPVLDFAFGASAYSLGPGAPPPPPPPPHSFYKQEPSWGAE 243
 90 PHEQCCLSAFTVHFSGQFTGTAGACRYGPGFPFPPPSQASSQARMFNAPVLPSCLESQP 149
 244 PHEQCCLSAFTVHFSGQFTGTAGACRYGPGFPFPPPSQASSQARMFNAPVLPSCLESQP 303

QY 150 AIRNOGYSTVTFDGTSPSYGHTPSHHAQFPNHSFKHEDPMGQGSGLGEQQYVPPPVYGC 209
 DB 304 AIRNOGYSTVTFDGTSPSYGHTPSHHAQFPNHSFKHEDPMGQGSGLGEQQYVPPPVYGC 363
 QY 210 HPTDSCGTSGQALLRLTPYSSDNLQMTSQLECMTNQNLGATLKG 256
 DB 364 HPTDSCGTSGQALLRLTPYSSDNLQMTSQLECMTNQNLGATLKG 410
 RESULT 9
 ADJ80768
 ID ADJ80768 standard; protein; 410 AA.
 XX
 AC ADJ80768;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 XX Wilm's tumor antigen associated protein #2.
 DE
 XX cytostatic; gene therapy; vaccine; Wilm's tumor antigen; Wt1; cancer;
 KW leukemia.
 XX
 OS Homo sapiens.
 XX
 PN WO2003037060-A2.
 XX
 PD 08-MAY-2003.
 XX
 PF 30-OCT-2002; 2002WO-US035194.
 XX
 PR 30-OCT-2001; 2001US-00002603.
 PR 16-APR-2002; 2002US-00125635.
 PR 12-JUL-2002; 2002US-00195835.
 PR 16-SEP-2002; 2002US-00244830.
 XX
 PA (CORI-) CORIXA CORP.
 PA (GAIG/) GAIGER A.
 XX
 PI Gaiger A, McNeill PD, Jaya N, Carter D;
 XX WPI; 2003-430453/40.
 DR
 XX New isolated polypeptide for diagnosing, preventing or treating malignant
 PT diseases, e.g. cancer or leukemia, comprises an immunogenic portion of a
 PT Wilm's tumor antigen.
 PT
 PS Disclosure; SEQ ID NO 333; 371pp; English.
 XX
 CC The invention relates to an isolated polypeptide comprising an
 CC immunogenic portion of a Wilm's tumor antigen, or its variant that
 CC differs in one or more substitutions, deletions, additions and/or
 CC insertions, such that the ability of the variant to react with Wt1-
 CC specific antisera and/or T-cell lines or clones is not substantially
 CC diminished. The composition and methods are useful in diagnosing,
 CC preventing or treating malignant diseases, such as cancer or leukemia.
 CC This sequence represents a protein of the invention.
 XX
 SQ Sequence 410 AA;
 Query Match 98.2%; Score 1418.5; DB 7; Length 410;
 Best Local Similarity 89.2%; Pred. No. 3.5e-102;
 Matches 256; Conservative 0; Mismatches 0; Indels 31; Gaps 1;
 1 MQHHHHH-----GSDVRDLNALLPAVPSLGGG 29
 124 MQHHHHHVTEGRASSGGGLVPRGSGGDDDDKSSRGSDVRDLNALLPAVPSLGGG 183
 30 GCALPVSGAAQWAPVLDFAFGASAYSLGPGAPPPPPPPPHSFYKQEPSWGAE 89
 184 GCALPVSGAAQWAPVLDFAFGASAYSLGPGAPPPPPPPPHSFYKQEPSWGAE 243
 90 PHEQCCLSAFTVHFSGQFTGTAGACRYGPGFPFPPPSQASSQARMFNAPVLPSCLESQP 149
 DB 244 PHEQCCLSAFTVHFSGQFTGTAGACRYGPGFPFPPPSQASSQARMFNAPVLPSCLESQP 303

```
Db 244 PHEOCLSAFTVHFSGQFTGTAGACRYGPFPPPSQASSQARMFNAPYLPSCLESQP 303
Qy 150 AIRNQGYSTVTFDGTSPSYGHTPSHHAQFPNHSFKHEDPMQOQSLGEGQQYSVPPPVYGC 209
Db 304 AIRNQGYSTVTFDGTSPSYGHTPSHHAQFPNHSFKHEDPMQOQSLGEGQQYSVPPPVYGC 363
Qy 210 HTPTDSTGSGQALLRTPYSSDNLQYMTSQLECMTNQMNIGATLKG 256
Db 364 HTPTDSTGSGQALLRTPYSSDNLQYMTSQLECMTNQMNIGATLKG 410

RESULT 10
ADJ83688
ID ADJ83688 standard; protein; 410 AA.
XX AC ADJ83688;
XX DT 06-MAY-2004 (first entry)
XX DE Human WT1 (Wilms tumour)-related Trx_WT1_A protein.
XX KW immune response; WT1; Wilms tumour; immunostimulant; cytostatic; vaccine;
XX KW malignant disease; leukaemia; cancer; human; Trx_WT1_A.
XX OS Homo sapiens.
XX OS Unidentified.
XX PN US2003235557-A1.
XX PD 25-DEC-2003.
XX PF 16-SEP-2002; 2002US-00244830.
XX PR 30-SEP-1998; 98US-00164223.
XX PR 25-MAR-1999; 99US-00276484.
XX PR 06-OCT-2000; 2000US-00684361.
XX PR 09-OCT-2000; 2000US-00685830.
XX PR 15-FEB-2001; 2001US-00785019.
XX PR 24-AUG-2001; 2001US-00938864.
XX PR 30-OCT-2001; 2001US-00002603.
XX PR 16-APR-2002; 2002US-00125635.
XX PR 12-JUL-2002; 2002US-00195835.
XX (CORI-) CORIXA CORP.
XX GA Gaiger A, Cheever MA;
XX WPI; 2004-070542/07.
XX N-PSDB; ADJ83683.
XX Inducing an immune response in an animal, useful for treating or
XX preventing cancer, comprises administering a composition comprising a
XX viral vector comprising an immunogenic portion of a WT1 polynucleotide.
XX Example 9; SEQ ID NO 333; 229pp; English.
XX The invention relates to a novel method for inducing an immune response
XX in an animal which involves administering a first and a second
XX composition comprising a first and a second viral vector, respectively,
XX each having at least an immunogenic portion of a WT1 (Wilms tumour)
XX polynucleotide operably linked to an expression control sequence. The
XX method of the invention has immunostimulant and cytostatic applications
XX and may be useful for generating or enhancing an immune response to WT1,
XX possibly via the production of a vaccine, as well as for preventing
XX and/or treating malignant diseases such as leukaemia and cancer. The
XX current sequence is that of the human WT1-related protein of the
XX invention.
XX SQ Sequence 410 AA;
```

Query Match 98.2%; Score 1418.5; DB 8; Length 410;
Best Local Similarity 89.2%; Pred. No. 3.5e-102;

```
Matches 256; Conservative 0; Mismatches 0; Indels 31; Gaps 1;
Qy 1 MQHHHHH-----GSDVRLNALLPAVPSLGGG 29
Db 124 MQHHHHHVSIIEGRASSGSGSLVPRGSSGDDDDKSSRGSDVRDLNALLPAVPSLGGG 183
Qy 30 GCALPVSGAAQWAPVLDFAFPGASAYGSLGGPAPPPPPPPPPPHSFIKQEPSWGAE 89
Db 184 GCALPVSGAAQWAPVLDFAFPGASAYGSLGGPAPPPPPPPPPPHSFIKQEPSWGAE 243
Qy 90 PHEOCLSAFTVHFSGQFTGTAGACRYGPFPPPSQASSQARMFNAPYLPSCLESQP 149
Db 244 PHEOCLSAFTVHFSGQFTGTAGACRYGPFPPPSQASSQARMFNAPYLPSCLESQP 303
Qy 150 AIRNQGYSTVTFDGTSPSYGHTPSHHAQFPNHSFKHEDPMQOQSLGEGQQYSVPPPVYGC 209
Db 304 AIRNQGYSTVTFDGTSPSYGHTPSHHAQFPNHSFKHEDPMQOQSLGEGQQYSVPPPVYGC 363
Qy 210 HTPTDSTGSGQALLRTPYSSDNLQYMTSQLECMTNQMNIGATLKG 256
Db 364 HTPTDSTGSGQALLRTPYSSDNLQYMTSQLECMTNQMNIGATLKG 410

RESULT 11
ADL57576
ID ADL57576 standard; protein; 410 AA.
XX AC ADL57576;
XX DT 20-MAY-2004 (first entry)
XX DE Human Trx-WT-1A fusion protein.
XX KW Human; Wilms' tumour; WT1; cancer; cytostatic; immunogen; antigen;
XX KW vaccine; T-cell; MHC; Major Histocompatibility Complex; HLA-A2;
XX KW human leukocyte antigen; Ral2; HIS tag; twin arginine translocator; TAT;
XX OS Malignant disease; fusion protein.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN US2003215458-A1.
XX PD 20-NOV-2003.
XX PF 30-OCT-2002; 2002US-00286333.
XX PR 30-SEP-1998; 98US-00164223.
XX PR 25-MAR-1999; 99US-00276484.
XX PR 06-OCT-2000; 2000US-00684361.
XX PR 09-OCT-2000; 2000US-00685830.
XX PR 15-FEB-2001; 2001US-00785019.
XX PR 24-AUG-2001; 2001US-00938864.
XX PR 30-OCT-2001; 2001US-00002603.
XX PR 16-APR-2002; 2002US-00125635.
XX PR 12-JUL-2002; 2002US-00195835.
XX PR 16-SEP-2002; 2002US-00244830.
XX (CORI-) CORIXA CORP.
XX GA Gaiger A, Mcneill PD, Jaya N;
XX WPI; 2004-021827/02.
XX N-PSDB; ADL57571.
XX New polypeptides and polynucleotides useful for generating or enhancing
XX an immune response to Wilms' tumor, or for treating and/or preventing
XX malignant diseases, e.g. cancer.
XX Example 9; SEQ ID NO 333; 259pp; English.
XX The invention relates to an isolated polypeptide comprising an
XX immunogenic portion of a Wilms' tumour antigen (WT1), or their variants
```

CC that differs in substitution(s), deletion(s), addition(s) and/or
CC insertion(s), where ability of the variant to react with Wt1-specific
CC antiserum and/or T-cell lines or clones is not substantially diminished.
CC Also included are a fusion protein comprising at least one Wt1
CC polypeptide, an isolated polynucleotide encoding the fusion protein, a
CC composition comprising a Wt1 polypeptide in combination with a
CC pharmaceutical carrier or excipient, a vaccine comprising a Wt1
CC polypeptide in combination with a non-specific immune response enhancer,
CC an expression vector comprising the polynucleotide operably linked to an
CC expression control sequence and a host cell transformed or transfected
CC with the expression vector. The immunogenic portion of the Wt1
CC polypeptide has been modified such that the ability of the immunogenic
CC portion to bind to an MHC (Major Histocompatibility Complex) molecule or
CC to HLA-A2 is increased relative to that of the immunogenic portion. The
CC Wt1 polypeptide may comprise a Wt1s' tumour antigen having a deletion of
CC a proline rich region at amino acid positions 54-68 of the Wt1s' tumour
CC antigen. The fusion partner is selected from Ral2, protein B, LYTA, a His
CC tag, a targeting signal capable of directing a polypeptide to the
CC endosomal/lysosomal compartment, twin arginine translocator (TAT), and
CC truncated twin arginine translocator. The polypeptide, polynucleotide or
CC compositions comprising them may be used for generating or enhancing an
CC immune response to Wt1s' tumour, and for treating and/or preventing
CC malignant diseases, e.g. cancer. The compositions may be used as markers
CC for the progression of cancer. The present sequence is a human Wt1-1
CC fusion protein sequence.

XX
SQ Sequence 410 AA;
Query Match 98.2%; Score 1418.5; DB 8; Length 410;
Best Local Similarity 89.2%; Pred. No. 3.5e-102;
Matches 256; Conservative 0; Mismatches 0; Indels 31; Gaps 1;
QY 1 MQHHHHH-----GSDVRLNALLPVPSLGGG 29
DB 124 MQHHHHHVSIEGRASSGGSLVPRGSGGDDDDKSSRGSDVRLNALLPVPSLGGG 183
QY 30 GCALPVSGAAQWAPVLDFAFPGASAYGSLGGPAPPPPPPPHSHFKQEPSSWGAE 89
DB 184 GCALPVSGAAQWAPVLDFAFPGASAYGSLGGPAPPPPPPPHSHFKQEPSSWGAE 243
QY 90 PHEQCCLSAFTVHFSGQFTGTAGACRYGPPGPPPPSQASSGQARMFPNAPYLPSCLESOP 149
DB 244 PHEQCCLSAFTVHFSGQFTGTAGACRYGPPGPPPPSQASSGQARMFPNAPYLPSCLESOP 303
QY 150 AIRNOGYSTVTFTDTPSYGHTPSHAAQFPNHSFKHEDPMGQGSGLGEQQYVSPPVYGC 209
DB 304 AIRNOGYSTVTFTDTPSYGHTPSHAAQFPNHSFKHEDPMGQGSGLGEQQYVSPPVYGC 363
QY 210 HTPDTSCTGSQALLLRTPYSSDNLQYMTSQCETWQNMNGLATLKG 256
DB 364 HTPDTSCTGSQALLLRTPYSSDNLQYMTSQCETWQNMNGLATLKG 410

RESULT 12
ADO09131
ID ADO09131 standard; protein; 410 AA.
XX
AC ADO09131;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human Trx_Wt1_A.
XX
KW Wt1s' tumour antigen; Wt1; vaccine; malignant disease; immunogenic;
XX leukaemia; cancer; human.
OS Homo sapiens.
XX
PN US2004018204-A1.
XX
PD 29-JAN-2004.
XX
PF 30-APR-2003; 2003US-00427717.

XX
PR 24-AUG-2001; 2001US-00938864.
PR 30-OCT-2001; 2001US-00002603.
PR 16-APR-2002; 2002US-00125635.
PR 12-JUL-2002; 2002US-00195835.
PR 16-SEP-2002; 2002US-00244830.
PR 30-OCT-2002; 2002US-00286333.
XX (CORI-) CORIXA CORP.
PA
XX Gaiger A, McNeill PD, Jaya N;
PI WPI; 2004-121992/12.
XX N-PSDB; ADO09126.
DR
XX New polypeptides and polynucleotides comprising an immunogenic portion of
PT a Wt1s' tumour antigen, useful as vaccines for preventing or treating
PT malignant diseases, e.g. cancer or leukemia.
XX
XX Example 9; SEQ ID NO 333; 252pp; English.
XX The invention relates to an isolated polypeptide which comprises an
CC immunogenic portion of a Wt1s' tumour antigen having a deletion of a
CC proline rich region, so that the ability of the variant to react with Wt1
CC -specific antiserum and/or T-cell lines or clones is not substantially
CC diminished. The polypeptide is useful as a vaccine in combination with a
CC non-specific immune response enhancer for preventing malignant diseases.
CC The polypeptide is useful for enhancing or inducing an immune response in
CC a patient; for inhibiting the development of malignant disease in a
CC patient; for stimulating or expanding T cells. The polypeptides,
CC polynucleotides and compositions are useful for treating malignant
CC diseases including leukaemia and cancer. The present sequence represents
CC the amino acid sequence of a human Wt1.
XX
SQ Sequence 410 AA;
Query Match 98.2%; Score 1418.5; DB 8; Length 410;
Best Local Similarity 89.2%; Pred. No. 3.5e-102;
Matches 256; Conservative 0; Mismatches 0; Indels 31; Gaps 1;
QY 1 MQHHHHH-----GSDVRLNALLPVPSLGGG 29
DB 124 MQHHHHHVSIEGRASSGGSLVPRGSGGDDDDKSSRGSDVRLNALLPVPSLGGG 183
QY 30 GCALPVSGAAQWAPVLDFAFPGASAYGSLGGPAPPPPPPPHSHFKQEPSSWGAE 89
DB 184 GCALPVSGAAQWAPVLDFAFPGASAYGSLGGPAPPPPPPPHSHFKQEPSSWGAE 243
QY 90 PHEQCCLSAFTVHFSGQFTGTAGACRYGPPGPPPPSQASSGQARMFPNAPYLPSCLESOP 149
DB 244 PHEQCCLSAFTVHFSGQFTGTAGACRYGPPGPPPPSQASSGQARMFPNAPYLPSCLESOP 303
QY 150 AIRNOGYSTVTFTDTPSYGHTPSHAAQFPNHSFKHEDPMGQGSGLGEQQYVSPPVYGC 209
DB 304 AIRNOGYSTVTFTDTPSYGHTPSHAAQFPNHSFKHEDPMGQGSGLGEQQYVSPPVYGC 363
QY 210 HTPDTSCTGSQALLLRTPYSSDNLQYMTSQCETWQNMNGLATLKG 256
DB 364 HTPDTSCTGSQALLLRTPYSSDNLQYMTSQCETWQNMNGLATLKG 410

RESULT 13
ABG33383
ID ABG33383 standard; protein; 591 AA.
XX
AC ABG33383;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human Trx_Wt1.
XX
KW Human; mouse; cytostatic; immunostimulant; Wt1; cancer; immune response.
XX


```
OS Homo sapiens.
XX WO200228414-A1.
XX 11-APR-2002.
XX 03-OCT-2001; 2001WO-US031139.
XX 06-OCT-2000; 2000US-00684361.
XX 09-OCT-2000; 2000US-00685830.
XX 15-FEB-2001; 2001US-00785019.
XX 24-AUG-2001; 2001US-00938864.
XX (CORI-) CORIXA CORP.
PA (GAIG/) GAIGER A.
XX
XX Gaiger A, McNeill PD, Smithgall M, Moulton G, Vedvick TS;
PI Sleath PR, Mossman S, Evans L, Spies AG, Boydston J;
XX WPI; 2002-352217/38.
XX N-PSDB; ABK69665.
XX
XX Novel isolated WT1 polynucleotide, and encoded polypeptide, useful for
PT treating and diagnosing cancer in a patient.
XX
XX Claim 2; Page 222-223; 260pp; English.
XX
XX The invention relates to an isolated WT1 polynucleotide (I) and
CC polypeptide encoded by (I). The WT1 polynucleotides and polypeptides are
CC used for treating and detecting cancer in a patient, and for stimulating
CC an immune response in patient. ABG33070-ABG33405 represent WT1 amino acid
CC sequences of the invention
XX
XX Sequence 591 AA;
SQ
Query Match 98.2%; Score 1419; DB 5; Length 591;
Best Local Similarity 88.9%; Pred. No. 5.8e-102;
Matches 256; Conservative 0; Mismatches 0; Indels 32; Gaps 1;
Qy 1 MQHHHHH-----GSDVRDLNALLPAVPSLGGG 28
Db 124 MQHHHHHVTEGRASSGSLVPRGSSGSDDDDKSSRMGSDVRDLNALLPAVPSLGGG 183
Qy 29 GGICALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPAPPPPPPHSFHKQSPSWGGA 88
Db 184 GGICALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPAPPPPPPHSFHKQSPSWGGA 243
Qy 89 EPHEEQCLSAFTVHFSGQFTGTAGACRYGPGPPPPPSQASGQARMFPNAPYLPSCLESQ 148
Db 244 EPHEEQCLSAFTVHFSGQFTGTAGACRYGPGPPPPPSQASGQARMFPNAPYLPSCLESQ 303
Qy 149 PAIRNQGYSTVTFDGTPTSYGHTPSHAAQPNHSHKEDPMGQGSGLGEQOQYVPPPPVYG 208
Db 304 PAIRNQGYSTVTFDGTPTSYGHTPSHAAQPNHSHKEDPMGQGSGLGEQOQYVPPPPVYG 363
Qy 209 CHTPTDCTGSQLLLRTPYSSDNLQYMTSLECMTNQNLGATLKG 256
Db 364 CHTPTDCTGSQLLLRTPYSSDNLQYMTSLECMTNQNLGATLKG 411
RESULT 14
ID ADB67536
XX ADB67536 standard; protein; 591 AA.
XX
XX ADB67536;
XX
XX 04-DEC-2003 (first entry)
XX
XX Human WT1-Trx fusion protein.
XX
XX Human; Wilm's tumour antigen; WT1; cytostatic; antigen; T cell;
KW antigen-presenting cell; CD4+; CD8+; immune response; cancer; vaccine;
KW leukaemia; antigen.
```

```
XX Synthetic.
OS Homo sapiens.
XX US2003072767-A1.
XX 17-APR-2003.
XX
XX 24-AUG-2001; 2001US-00938864.
XX
XX 30-SEP-1998; 98US-00164223.
XX 25-MAR-1999; 99US-00276484.
XX 06-OCT-2000; 2000US-00684361.
XX 09-OCT-2000; 2000US-00685830.
XX 15-FEB-2001; 2001US-00785019.
XX
XX (GAIG/) GAIGER A.
XX (MCNEI/) MCNEILL P D.
XX (SMIT/) SMITHGALL M.
XX (MOUL/) MOULTON G.
XX (VEDV/) VEDVICK T S.
XX (SLEA/) SLEATH P R.
XX (MOSS/) MOSSMAN S.
XX (EVAN/) EVANS L.
XX (SPIE/) SPIES A G.
XX (BOYD/) BOYDSTON J.
XX
XX Gaiger A, McNeill PD, Smithgall M, Moulton G, Vedvick TS;
PI Sleath PR, Mossman S, Evans L, Spies AG, Boydston J;
XX WPI; 2003-605957/57.
XX N-PSDB; ADB67531.
XX
XX Novel Wilms tumor polynucleotides encoding WT1 polypeptides, useful for
PT detecting the presence of cancer in a patient, and in pharmaceutical
XX compositions, e.g. vaccines, for treating cancers e.g. leukemia.
XX
XX Claim 2; Page 125-127; 197pp; English.
XX
XX The invention relates to an isolated Wilm tumour (WT1) polynucleotide
CC comprising a full length protein, truncated protein, mutated protein or
CC fusion protein. Also included are the encoded WT1 proteins, expression
CC vectors, host cells, antibodies, detecting the presence of a cancer in a
CC patient by contacting a biological sample with a binding agent that binds
CC to a WT1 protein, an oligonucleotide that hybridises to a WT1
CC polynucleotide, stimulating and/or expanding T cells specific for a
CC tumour protein by contacting T cells with the WT1 polynucleotide, the WT1
CC protein or antigen-presenting cells that express the WT1 protein, a
CC composition (C1) (comprising physiologically acceptable carriers and
CC immunostimulants as first component, and a second component selected from
CC the WT1 polynucleotide, the WT1 protein, Ab, or T cells and antigen
CC presenting cells that express the WT1 protein), inhibiting the
CC development of a cancer in a patient (by incubating CD4+ and/or CD8+ T
CC cells isolated from a patient with the WT1 polynucleotide, the WT1
CC protein or antigen presenting cells that express the WT1 protein, such
CC that T cell proliferate, administering the proliferated T cells to the
CC patient, and thus inhibiting the development of a cancer in the patient)
CC and a composition (C2) (comprising a WT1 polypeptide resuspended in a
CC buffer comprising at least 1-3 sugars selected from trehalose, maltose,
CC sucrose, fructose and glucose, at a concentration of 7-13%, and
CC optionally ethanolamine, cysteine and Polysorbate-80, or WT1 polypeptide
CC and MPL-SE or Enhazyn). Also disclosed as anew are polypeptides
CC comprising a variant of an immunogenic portion of WT1 polypeptide. C1 is
CC useful for stimulating immune response in a patient, and for treating
CC cancer in a patient. The oligonucleotide is also useful for determining
CC the presence of a cancer in a patient. The WT1 polynucleotide and the WT1
CC protein are useful in pharmaceutical compositions, e.g. vaccines. The WT1
CC protein is useful as marker to indicate the presence or absence of a
CC cancer. C1 is useful for inhibiting the development of a malignant
CC disease in a patient, for preventing and treating metastatic diseases
CC e.g. leukaemia and cancer, and for removing tumour cells from a
CC biological sample. Ab (binding agent for the WT1 protein) is useful for
CC detecting the presence of cancer in a patient. The present sequence
```

CC represents a Human WT1 fusion protein.

XX Sequence 591 AA;

Query Match 98.2%; Score 1418; DB 7; Length 591;
Best Local Similarity 88.9%; Pred. No. 5.8e-102;
Matches 256; Conservative 0; Mismatches 0; Indels 32; Gaps 1;
QY 1 MQHHHHH-----GSDVRLNALLPAVPSLGGG 28
DB 124 MQHHHHHVSIEGRASGGSLVPRGSSGGDDDDKSSRMGSDVRLNALLPAVPSLGGG 183
QY 29 GGCAIPVSGAAQWAPVLDFAAPPGASAYGSLGGPAPPAPPPPPPHSFIIKQEPSWGGA 88
DB 184 GGCAIPVSGAAQWAPVLDFAAPPGASAYGSLGGPAPPAPPPPPPHSFIIKQEPSWGGA 243
QY 89 EPHEEQCLSAFTVHFSQGTGTAGACRYGPGPPPSQASSGQARMFPNAPYLPSCLESQ 148
DB 244 EPHEEQCLSAFTVHFSQGTGTAGACRYGPGPPPSQASSGQARMFPNAPYLPSCLESQ 303
QY 149 PAIRNOGYSTVTFDGTSPSYGHTPSHAAQFPNHSFKHEDPMGQGSGLGEQOQYSVPPPVY 208
DB 304 PAIRNOGYSTVTFDGTSPSYGHTPSHAAQFPNHSFKHEDPMGQGSGLGEQOQYSVPPPVY 363
QY 209 CHTPTDCTGSQLLLRTPYSSDNLQYMTSQLECMTNQNLGATLKG 256
DB 364 CHTPTDCTGSQLLLRTPYSSDNLQYMTSQLECMTNQNLGATLKG 411

RESULT 15

ADJ80769
ID ADJ80769 standard; protein; 591 AA.

AC ADJ80769;

DT 06-MAY-2004 (first entry)

XX Wilm's tumor antigen associated protein #3.

XX cytostatic; gene therapy; vaccine; Wilm's tumor antigen; WT1; cancer;
KW leukemia.

XX Homo sapiens.

XX WO2003037060-A2.

XX 08-MAY-2003.

XX 30-OCT-2002; 2002WO-US035194.

XX 30-OCT-2001; 2001US-00002603.

PR 16-APR-2002; 2002US-00125635.

PR 12-JUL-2002; 2002US-00195835.

PR 16-SEP-2002; 2002US-00244830.

XX (CORI-) CORIXA CORP.

PA (GAIG/) GAIGER A.

XX Gaiger A, McNeill PD, Jaya N, Carter D;

XX WPI; 2003-430453/40.

XX New isolated polypeptide for diagnosing, preventing or treating malignant

XX diseases, e.g. cancer or leukemia, comprises an immunogenic portion of a

XX Wilm's tumor antigen.

XX Disclosure; SEQ ID NO 334; 371pp; English.

XX The invention relates to an isolated polypeptide comprising an

XX immunogenic portion of a Wilm's tumor antigen, or its variant that

XX differs in one or more substitutions, deletions, additions and/or

CC diminished. The composition and methods are useful in diagnosing,
CC preventing or treating malignant diseases, such as cancer or leukemia.
CC This sequence represents a protein of the invention.

XX Sequence 591 AA;

Query Match 98.2%; Score 1418; DB 7; Length 591;
Best Local Similarity 88.9%; Pred. No. 5.8e-102;
Matches 256; Conservative 0; Mismatches 0; Indels 32; Gaps 1;
QY 1 MQHHHHH-----GSDVRLNALLPAVPSLGGG 28
DB 124 MQHHHHHVSIEGRASGGSLVPRGSSGGDDDDKSSRMGSDVRLNALLPAVPSLGGG 183
QY 29 GGCAIPVSGAAQWAPVLDFAAPPGASAYGSLGGPAPPAPPPPPPHSFIIKQEPSWGGA 88
DB 184 GGCAIPVSGAAQWAPVLDFAAPPGASAYGSLGGPAPPAPPPPPPHSFIIKQEPSWGGA 243
QY 89 EPHEEQCLSAFTVHFSQGTGTAGACRYGPGPPPSQASSGQARMFPNAPYLPSCLESQ 148
DB 244 EPHEEQCLSAFTVHFSQGTGTAGACRYGPGPPPSQASSGQARMFPNAPYLPSCLESQ 303
QY 149 PAIRNOGYSTVTFDGTSPSYGHTPSHAAQFPNHSFKHEDPMGQGSGLGEQOQYSVPPPVY 208
DB 304 PAIRNOGYSTVTFDGTSPSYGHTPSHAAQFPNHSFKHEDPMGQGSGLGEQOQYSVPPPVY 363
QY 209 CHTPTDCTGSQLLLRTPYSSDNLQYMTSQLECMTNQNLGATLKG 256
DB 364 CHTPTDCTGSQLLLRTPYSSDNLQYMTSQLECMTNQNLGATLKG 411

Search completed: May 10, 2005, 18:41:49

Job time : 168 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 10, 2005, 18:36:50 ; Search time 43 Seconds
(without alignments)
444.422 Million cell updates/sec

Title: US-09-785-019B-335

Perfect score: 1444

Sequence: 1 MQHHHHHGGSDVRLNALLP.....TSQLECMWNQMLGATLKG 256

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1386	96.0	429	1	US-08-234-783-4
2	1386	96.0	429	1	US-08-456-907-4
3	1386	96.0	429	5	PCT-US95-05523-4
4	1386	96.0	449	1	US-08-102-942A-6
5	1386	96.0	449	3	US-08-037-179B-6
6	1386	96.0	449	4	US-09-538-092-960
7	1386	96.0	449	4	US-09-949-016-9138
8	1386	96.0	559	4	US-08-949-016-9139
9	1386	96.0	559	4	US-09-949-016-9140
10	1386	96.0	559	4	US-09-949-016-9141
11	1386	96.0	576	4	US-09-949-016-9404
12	1386	96.0	576	4	US-09-949-016-9405
13	1386	96.0	576	4	US-09-949-016-9406
14	1386	96.0	576	4	US-09-949-016-9407
15	1329	92.0	449	1	US-08-102-942A-4
16	1329	92.0	449	3	US-09-037-179B-4
17	1051	72.8	210	1	US-08-234-783-2
18	1051	72.8	210	1	US-08-456-907-2
19	1051	72.8	210	5	PCT-US95-05523-2
20	917	63.5	345	1	US-08-102-942A-2
21	917	63.5	345	3	US-09-037-179B-2
22	849	58.8	154	1	US-08-102-942A-5
23	849	58.8	154	3	US-09-037-179B-5
24	140	9.7	503	4	US-09-949-016-9746
25	139	9.6	1274	3	US-09-095-443-2
26	138.5	9.6	971	4	US-09-538-092-1332
27	135.5	9.4	945	4	US-09-248-796A-15743

28 135.5 9.4 1007 4 US-10-144-198-36 Sequence 36, Appl
29 135.5 9.4 1041 4 US-10-144-198-14 Sequence 14, Appl
30 135 9.3 707 4 US-09-919-039-278 Sequence 278, App
31 135 9.3 707 4 US-09-538-092-993 Sequence 993, App
32 135 9.3 735 4 US-09-949-016-10120 Sequence 10120, A
33 135 9.3 1315 3 US-08-899-595-3 Sequence 3, Appl
34 134 9.3 780 4 US-09-949-016-10205 Sequence 10205, A
35 134 9.3 1184 4 US-09-266-225D-18 Sequence 18, Appl
36 133 9.2 684 4 US-09-823-240A-9 Sequence 9, Appl
37 133 9.2 1248 2 US-09-080-897-2 Sequence 2, Appl
38 133 9.2 1248 3 US-09-323-735-2 Sequence 2, Appl
39 129.5 9.0 693 4 US-09-949-016-7806 Sequence 23, Appl
40 129.5 9.0 1185 3 US-09-041-886-23 Sequence 1209, Ap
41 129.5 9.0 1185 4 US-09-538-092-1209 Sequence 4, Appl
42 129 8.9 345 1 US-08-031-148-4 Sequence 4, Appl
43 129 8.9 345 3 US-08-415-838-4 Sequence 4, Appl
44 129 8.9 345 3 US-09-205-169-4 Sequence 4, Appl
45 129 8.9 697 4 US-09-949-016-9660 Sequence 9660, Ap

ALIGNMENTS

RESULT 1
US-08-234-783-4
; Sequence 4, Application US/08234783
; Patent No. 5622835
; GENERAL INFORMATION:
; APPLICANT: Herlyn, Meenhard
; APPLICANT: Morris, Jennifer
; APPLICANT: Rauscher III, Frank J.
; APPLICANT: Rodeck, Ulrich
; TITLE OF INVENTION: Wt1 Monoclonal Antibodies and Methods of
; TITLE OF INVENTION: Use Therefor
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Cntr, PO Box 457
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/234,783
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: WST48USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9200
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 429 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-234-783-4

Query Match 96.0%; Score 1386; DB 1; Length 429;
Best Local Similarity 100.0%; Pred. No. 1.3e-110;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 9 GSDVRDNLNALLPAVPSLGGGGGCGALPVSGAAQWAPVLDFAFPAGASAYGSLGGPAPP 68
Db 2 GSDVRDNLNALLPAVPSLGGGGGCGALPVSGAAQWAPVLDFAFPAGASAYGSLGGPAPP 61

QY 69 PPPPPPHSFIKQEPWSGGAEPHEQCCLSAFTVHFSQFTGTAGACRYGPGFPPPSQAS 128
| | | | |
Db 62 PPPPPPHSFIKQEPWSGGAEPHEQCCLSAFTVHFSQFTGTAGACRYGPGFPPPSQAS 121
| | | | |
QY 129 SGQARFNPAPYLPSCLESQPAIRNOGYSTVTFDGTSPSYGHTPSHAAQFPNHSFKHEDP 188
| | | | |
Db 122 SGQARFNPAPYLPSCLESQPAIRNOGYSTVTFDGTSPSYGHTPSHAAQFPNHSFKHEDP 181
| | | | |
QY 189 MGQOQSLGEOQYVPPPVYGGHTPTDSCGSAQALLRTPYSSDNLQMTSOLECMTWNQ 248
| | | | |
Db 182 MGQOQSLGEOQYVPPPVYGGHTPTDSCGSAQALLRTPYSSDNLQMTSOLECMTWNQ 241
| | | | |
QY 249 NLGATLKG 256
| | | | |
Db 242 NLGATLKG 249
| | | | |

RESULT 2
US-08-456-907-4
; Sequence 4, Application US/08456907
; Patent No. 5633142
; GENERAL INFORMATION:
; APPLICANT: Herlyn, Meenhard
; APPLICANT: Morris, Jennifer
; APPLICANT: Rauscher III, Frank J.
; APPLICANT: Rodeck, Ulrich
; TITLE OF INVENTION: Wt1 Monoclonal Antibodies and Methods of
; TITLE OF INVENTION: Use Therefor
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Cntr, PO Box 457
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/456,907
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/234,783
; FILING DATE: 28-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: WST48AUSA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9200
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 429 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-456-907-4

Query Match 96.0%; Score 1386; DB 1; Length 429;
Best Local Similarity 100.0%; Pred. No. 1.3e-110;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 GSDVRDLNALLPAVPSLGGGGGCGALPVSGAAQWAPVLDFAAPPASAYGSLGGPAPPAPP 68
| | | | |
Db 2 GSDVRDLNALLPAVPSLGGGGGCGALPVSGAAQWAPVLDFAAPPASAYGSLGGPAPPAPP 61
| | | | |
QY 69 PPPPPPHSFIKQEPWSGGAEPHEQCCLSAFTVHFSQFTGTAGACRYGPGFPPPSQAS 128
| | | | |
Db 2 GSDVRDLNALLPAVPSLGGGGGCGALPVSGAAQWAPVLDFAAPPASAYGSLGGPAPPAPP 61
| | | | |
QY 69 PPPPPPHSFIKQEPWSGGAEPHEQCCLSAFTVHFSQFTGTAGACRYGPGFPPPSQAS 128
| | | | |

Db 62 PPPPPPHSFIKQEPWSGGAEPHEQCCLSAFTVHFSQFTGTAGACRYGPGFPPPSQAS 121
| | | | |
QY 129 SGQARFNPAPYLPSCLESQPAIRNOGYSTVTFDGTSPSYGHTPSHAAQFPNHSFKHEDP 188
| | | | |
Db 122 SGQARFNPAPYLPSCLESQPAIRNOGYSTVTFDGTSPSYGHTPSHAAQFPNHSFKHEDP 181
| | | | |
QY 189 MGQOQSLGEOQYVPPPVYGGHTPTDSCGSAQALLRTPYSSDNLQMTSOLECMTWNQ 248
| | | | |
Db 182 MGQOQSLGEOQYVPPPVYGGHTPTDSCGSAQALLRTPYSSDNLQMTSOLECMTWNQ 241
| | | | |
QY 249 NLGATLKG 256
| | | | |
Db 242 NLGATLKG 249
| | | | |

RESULT 3
PCT-US95-05523-4
; Sequence 4, Application PC/TUS9505523
; GENERAL INFORMATION:
; APPLICANT: The Wistar Institute of Anatomy and Biology
; TITLE OF INVENTION: Wt1 Monoclonal Antibodies and
; TITLE OF INVENTION: Methods of Use Therefor
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Cntr, PO Box 457
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/05523
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: US 08/234,783
; APPLICATION NUMBER: US 08/234,783
; FILING DATE: 28-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: WST48PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9200
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 429 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-05523-4

Query Match 96.0%; Score 1386; DB 5; Length 429;
Best Local Similarity 100.0%; Pred. No. 1.3e-110;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 GSDVRDLNALLPAVPSLGGGGGCGALPVSGAAQWAPVLDFAAPPASAYGSLGGPAPPAPP 68
| | | | |
Db 2 GSDVRDLNALLPAVPSLGGGGGCGALPVSGAAQWAPVLDFAAPPASAYGSLGGPAPPAPP 61
| | | | |
QY 69 PPPPPPHSFIKQEPWSGGAEPHEQCCLSAFTVHFSQFTGTAGACRYGPGFPPPSQAS 128
| | | | |
Db 62 PPPPPPHSFIKQEPWSGGAEPHEQCCLSAFTVHFSQFTGTAGACRYGPGFPPPSQAS 121
| | | | |
QY 129 SGQARFNPAPYLPSCLESQPAIRNOGYSTVTFDGTSPSYGHTPSHAAQFPNHSFKHEDP 188
| | | | |
Db 122 SGQARFNPAPYLPSCLESQPAIRNOGYSTVTFDGTSPSYGHTPSHAAQFPNHSFKHEDP 181
| | | | |

QY 189 MGQGSILGEQOQSVPPVYCHTPTDSCSQALLLRTPTSSDNLRYQMTSOLECMTWNQM 248
Db 182 MGQGSILGEQOQSVPPVYCHTPTDSCSQALLLRTPTSSDNLRYQMTSOLECMTWNQM 241
QY 249 NLGATLKG 256
Db 242 NLGATLKG 249

RESULT 4

US-08-102-942A-6
; Sequence 6, Application US/08102942A
; Patent No. 5728288
; GENERAL INFORMATION:
; APPLICANT: Call, Katherine M.
; APPLICANT: Glaser, Thomas M.
; APPLICANT: Ito, Caryn Y.
; APPLICANT: Buckler, Alan J.
; APPLICANT: Pelletier, Jerry
; APPLICANT: Rose, Elise A.
; APPLICANT: Housman, David E.
; APPLICANT: Bruening, Wendy
; APPLICANT: Darveau, Andre
; TITLE OF INVENTION: Localization and Characterization of the
; TITLE OF INVENTION: Wilms' Tumor Gene
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.
; ZIP: 02173
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/102,942A
; FILING DATE: 02-AUG-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: MIT-5194A2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 449 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-102-942A-6

Query Match 96.0%; Score 1386; DB 1; Length 449;
Best Local Similarity 100.0%; Pred. No. 1.4e-110;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GSDVRDLNALLPAVPSLGGGGGCGALPVSGAAQWAPVLDFAPPASAYGSLGGPAPP 68
Db 2 GSDVRDLNALLPAVPSLGGGGGCGALPVSGAAQWAPVLDFAPPASAYGSLGGPAPP 61
QY 69 PPPPPPHSFIKQPSWGGGAEPHEEOCLSAFTVHFSQQTGTAGACRYGFGPPPPSQAS 128
Db 62 PPPPPPHSFIKQPSWGGGAEPHEEOCLSAFTVHFSQQTGTAGACRYGFGPPPPSQAS 121
QY 129 SGQARMPFNAPYLPSCLESQPAIRNOGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDP 188

Db 122 SGQARMPFNAPYLPSCLESQPAIRNOGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDP 181
QY 189 MGQGSILGEQOQSVPPVYCHTPTDSCSQALLLRTPTSSDNLRYQMTSOLECMTWNQM 248
Db 182 MGQGSILGEQOQSVPPVYCHTPTDSCSQALLLRTPTSSDNLRYQMTSOLECMTWNQM 241
QY 249 NLGATLKG 256
Db 242 NLGATLKG 249

RESULT 5

US-09-037-179B-6
; Sequence 6, Application US/09037179B
; Patent No. 6316599
; GENERAL INFORMATION:
; APPLICANT: Call, Katherine M.
; APPLICANT: Glaser, Thomas M.
; APPLICANT: Ito, Caryn Y.
; APPLICANT: Buckler, Alan J.
; APPLICANT: Pelletier, Jerry
; APPLICANT: Haber, Daniel A.
; APPLICANT: Rose, Elise A.
; APPLICANT: Housman, David E.
; APPLICANT: Bruening, Wendy
; APPLICANT: Darveau, Andre
; TITLE OF INVENTION: Localization and Characterization of the
; TITLE OF INVENTION: Wilms' Tumor Gene
; FILE REFERENCE: 0050.1312-011
; CURRENT APPLICATION NUMBER: US/09/037,179B
; CURRENT FILING DATE: 1998-03-09
; PRIOR APPLICATION NUMBER: US 08/102,942
; PRIOR FILING DATE: 1993-08-02
; PRIOR APPLICATION NUMBER: US 07/614,161
; PRIOR FILING DATE: 1990-11-13
; PRIOR APPLICATION NUMBER: US 07/435,780
; PRIOR FILING DATE: 1989-11-13
; PRIOR APPLICATION NUMBER: US 07/795,323
; PRIOR FILING DATE: 1994-09-27
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-037-179B-6

Query Match 96.0%; Score 1386; DB 3; Length 449;
Best Local Similarity 100.0%; Pred. No. 1.4e-110;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GSDVRDLNALLPAVPSLGGGGGCGALPVSGAAQWAPVLDFAPPASAYGSLGGPAPP 68
Db 2 GSDVRDLNALLPAVPSLGGGGGCGALPVSGAAQWAPVLDFAPPASAYGSLGGPAPP 61
QY 69 PPPPPPHSFIKQPSWGGGAEPHEEOCLSAFTVHFSQQTGTAGACRYGFGPPPPSQAS 128
Db 62 PPPPPPHSFIKQPSWGGGAEPHEEOCLSAFTVHFSQQTGTAGACRYGFGPPPPSQAS 121
QY 129 SGQARMPFNAPYLPSCLESQPAIRNOGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDP 188
Db 122 SGQARMPFNAPYLPSCLESQPAIRNOGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDP 181
QY 189 MGQGSILGEQOQSVPPVYCHTPTDSCSQALLLRTPTSSDNLRYQMTSOLECMTWNQM 248
Db 182 MGQGSILGEQOQSVPPVYCHTPTDSCSQALLLRTPTSSDNLRYQMTSOLECMTWNQM 241
QY 249 NLGATLKG 256
Db 242 NLGATLKG 249

```
RESULT 6
US-09-538-092-960
; Sequence 960, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurapacSeqFormatter Version 0.9
; SEQ ID NO 960
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Polypeptide Accession Number P19544
US-09-538-092-960

Query Match          96.0%; Score 1386; DB 4; Length 449;
Best Local Similarity 100.0%; Pred. No. 1.4e-110;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  9 GSDVDLNALLPAVPSLGGGGGCGALPVSGAAQWAPVLDFAAPPASAYGSLGGPAPPAPP 68
DB  2 GSDVDLNALLPAVPSLGGGGGCGALPVSGAAQWAPVLDFAAPPASAYGSLGGPAPPAPP 61
QY  69 PPPPPPHSFHIKQEPSWGGAEPHEEOCLSAFTVHFSQQTGTAGACRYGFGPPPPPSQAS 128
DB  62 PPPPPPHSFHIKQEPSWGGAEPHEEOCLSAFTVHFSQQTGTAGACRYGFGPPPPPSQAS 121
QY  129 SGQARMPFNAPYLPSCLESQPAIRNQGYSYTVFDGTPSYGHTPSHAAQFPNHSFKHEDP 188
DB  122 SGQARMPFNAPYLPSCLESQPAIRNQGYSYTVFDGTPSYGHTPSHAAQFPNHSFKHEDP 181
QY  189 MGQGSGLGEQQYSVPPPVYGGCHTPTDSCGQALLLRTPYSSDNLQYMTSQLECMWTNQ 248
DB  182 MGQGSGLGEQQYSVPPPVYGGCHTPTDSCGQALLLRTPYSSDNLQYMTSQLECMWTNQ 241
QY  249 NLGATLKG 256
DB  242 NLGATLKG 249

RESULT 7
US-09-949-016-9138
; Sequence 9138, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9138
; LENGTH: 559
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9138

Query Match          96.0%; Score 1386; DB 4; Length 559;
Best Local Similarity 100.0%; Pred. No. 1.8e-110;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  9 GSDVDLNALLPAVPSLGGGGGCGALPVSGAAQWAPVLDFAAPPASAYGSLGGPAPPAPP 68
DB  132 GSDVDLNALLPAVPSLGGGGGCGALPVSGAAQWAPVLDFAAPPASAYGSLGGPAPPAPP 191
QY  69 PPPPPPHSFHIKQEPSWGGAEPHEEOCLSAFTVHFSQQTGTAGACRYGFGPPPPPSQAS 128
DB  192 PPPPPPHSFHIKQEPSWGGAEPHEEOCLSAFTVHFSQQTGTAGACRYGFGPPPPPSQAS 251
QY  129 SGQARMPFNAPYLPSCLESQPAIRNQGYSYTVFDGTPSYGHTPSHAAQFPNHSFKHEDP 188
DB  252 SGQARMPFNAPYLPSCLESQPAIRNQGYSYTVFDGTPSYGHTPSHAAQFPNHSFKHEDP 311
QY  189 MGQGSGLGEQQYSVPPPVYGGCHTPTDSCGQALLLRTPYSSDNLQYMTSQLECMWTNQ 248
DB  312 MGQGSGLGEQQYSVPPPVYGGCHTPTDSCGQALLLRTPYSSDNLQYMTSQLECMWTNQ 371
```

```
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9138

Query Match          96.0%; Score 1386; DB 4; Length 559;
Best Local Similarity 100.0%; Pred. No. 1.8e-110;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  9 GSDVDLNALLPAVPSLGGGGGCGALPVSGAAQWAPVLDFAAPPASAYGSLGGPAPPAPP 68
DB  132 GSDVDLNALLPAVPSLGGGGGCGALPVSGAAQWAPVLDFAAPPASAYGSLGGPAPPAPP 191
QY  69 PPPPPPHSFHIKQEPSWGGAEPHEEOCLSAFTVHFSQQTGTAGACRYGFGPPPPPSQAS 128
DB  192 PPPPPPHSFHIKQEPSWGGAEPHEEOCLSAFTVHFSQQTGTAGACRYGFGPPPPPSQAS 251
QY  129 SGQARMPFNAPYLPSCLESQPAIRNQGYSYTVFDGTPSYGHTPSHAAQFPNHSFKHEDP 188
DB  252 SGQARMPFNAPYLPSCLESQPAIRNQGYSYTVFDGTPSYGHTPSHAAQFPNHSFKHEDP 311
QY  189 MGQGSGLGEQQYSVPPPVYGGCHTPTDSCGQALLLRTPYSSDNLQYMTSQLECMWTNQ 248
DB  312 MGQGSGLGEQQYSVPPPVYGGCHTPTDSCGQALLLRTPYSSDNLQYMTSQLECMWTNQ 371

RESULT 8
US-09-949-016-9139
; Sequence 9139, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9139
; LENGTH: 559
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9139

Query Match          96.0%; Score 1386; DB 4; Length 559;
Best Local Similarity 100.0%; Pred. No. 1.8e-110;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  9 GSDVDLNALLPAVPSLGGGGGCGALPVSGAAQWAPVLDFAAPPASAYGSLGGPAPPAPP 68
DB  132 GSDVDLNALLPAVPSLGGGGGCGALPVSGAAQWAPVLDFAAPPASAYGSLGGPAPPAPP 191
QY  69 PPPPPPHSFHIKQEPSWGGAEPHEEOCLSAFTVHFSQQTGTAGACRYGFGPPPPPSQAS 128
DB  192 PPPPPPHSFHIKQEPSWGGAEPHEEOCLSAFTVHFSQQTGTAGACRYGFGPPPPPSQAS 251
QY  129 SGQARMPFNAPYLPSCLESQPAIRNQGYSYTVFDGTPSYGHTPSHAAQFPNHSFKHEDP 188
DB  252 SGQARMPFNAPYLPSCLESQPAIRNQGYSYTVFDGTPSYGHTPSHAAQFPNHSFKHEDP 311
QY  189 MGQGSGLGEQQYSVPPPVYGGCHTPTDSCGQALLLRTPYSSDNLQYMTSQLECMWTNQ 248
DB  312 MGQGSGLGEQQYSVPPPVYGGCHTPTDSCGQALLLRTPYSSDNLQYMTSQLECMWTNQ 371
```

```
Qy 249 NLGATLKG 256
Db 372 NLGATLKG 379

RESULT 9
US-09-949-016-9140
; Sequence 9140, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9140
; LENGTH: 559
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9140

Query Match 96.0%; Score 1386; DB 4; Length 559;
Best Local Similarity 100.0%; Pred. No. 1.8e-110;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GSDVRDLNALLPAVPSLGGGGCCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPP 68
Db 132 GSDVRDLNALLPAVPSLGGGGCCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPP 191
Qy 69 PPPPPPHSFIKQEPSWGGAEPEHEEQCLSAFTVHFSQQTGTAGACRYGFGPPPPSOAS 128
Db 192 PPPPPPHSFIKQEPSWGGAEPEHEEQCLSAFTVHFSQQTGTAGACRYGFGPPPPSOAS 251
Qy 129 SQQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTSPSYGHTPSHHAQFPNHSFKHEDP 188
Db 252 SQQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTSPSYGHTPSHHAQFPNHSFKHEDP 311
Qy 189 MGQGSGLGEQOYSVPPPVYGCHTPTDSCGSOALLLRTPTSSDNLQYMTSQCMTWNQM 248
Db 312 MGQGSGLGEQOYSVPPPVYGCHTPTDSCGSOALLLRTPTSSDNLQYMTSQCMTWNQM 371
Qy 249 NLGATLKG 256
Db 372 NLGATLKG 379

RESULT 11
US-09-949-016-9404
; Sequence 9404, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9404
; LENGTH: 576
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9404

Query Match 96.0%; Score 1386; DB 4; Length 576;
Best Local Similarity 100.0%; Pred. No. 1.9e-110;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GSDVRDLNALLPAVPSLGGGGCCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPP 68
Db 132 GSDVRDLNALLPAVPSLGGGGCCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPP 191
Qy 69 PPPPPPHSFIKQEPSWGGAEPEHEEQCLSAFTVHFSQQTGTAGACRYGFGPPPPSOAS 128
Db 192 PPPPPPHSFIKQEPSWGGAEPEHEEQCLSAFTVHFSQQTGTAGACRYGFGPPPPSOAS 251
Qy 129 SQQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTSPSYGHTPSHHAQFPNHSFKHEDP 188
Db 252 SQQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTSPSYGHTPSHHAQFPNHSFKHEDP 311
```

```
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9141
; LENGTH: 559
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9141

Query Match 96.0%; Score 1386; DB 4; Length 559;
Best Local Similarity 100.0%; Pred. No. 1.8e-110;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GSDVRDLNALLPAVPSLGGGGCCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPP 68
Db 132 GSDVRDLNALLPAVPSLGGGGCCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPP 191
Qy 69 PPPPPPHSFIKQEPSWGGAEPEHEEQCLSAFTVHFSQQTGTAGACRYGFGPPPPSOAS 128
Db 192 PPPPPPHSFIKQEPSWGGAEPEHEEQCLSAFTVHFSQQTGTAGACRYGFGPPPPSOAS 251
Qy 129 SQQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTSPSYGHTPSHHAQFPNHSFKHEDP 188
Db 252 SQQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTSPSYGHTPSHHAQFPNHSFKHEDP 311
Qy 189 MGQGSGLGEQOYSVPPPVYGCHTPTDSCGSOALLLRTPTSSDNLQYMTSQCMTWNQM 248
Db 312 MGQGSGLGEQOYSVPPPVYGCHTPTDSCGSOALLLRTPTSSDNLQYMTSQCMTWNQM 371
Qy 249 NLGATLKG 256
Db 372 NLGATLKG 379

RESULT 11
US-09-949-016-9404
; Sequence 9404, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9404
; LENGTH: 576
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9404

Query Match 96.0%; Score 1386; DB 4; Length 576;
Best Local Similarity 100.0%; Pred. No. 1.9e-110;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GSDVRDLNALLPAVPSLGGGGCCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPP 68
Db 132 GSDVRDLNALLPAVPSLGGGGCCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPP 191
Qy 69 PPPPPPHSFIKQEPSWGGAEPEHEEQCLSAFTVHFSQQTGTAGACRYGFGPPPPSOAS 128
Db 192 PPPPPPHSFIKQEPSWGGAEPEHEEQCLSAFTVHFSQQTGTAGACRYGFGPPPPSOAS 251
Qy 129 SQQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTSPSYGHTPSHHAQFPNHSFKHEDP 188
Db 252 SQQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTSPSYGHTPSHHAQFPNHSFKHEDP 311
```

```

QY 189 MGQGSIGEQQYVPPPPVYCHTPTDSCGQALLLRTPYSSDNLXQMTSOLCMTWNQM 248
Db 312 MGQGSIGEQQYVPPPPVYCHTPTDSCGQALLLRTPYSSDNLXQMTSOLCMTWNQM 371

QY 249 NLGATLKG 256
Db 372 NLGATLKG 379

RESULT 12
US-09-949-016-9405
; Sequence 9405, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9405
; LENGTH: 576
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-9405

Query Match 96.0%; Score 1386; DB 4; Length 576;
Best Local Similarity 100.0%; Pred. No. 1.9e-110;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GSDVRDLNALLPAVPSLGGGGGCGALPVSGAAQWAPVLDFAAPGASAYGSLGGAPPAPP 68
Db 132 GSDVRDLNALLPAVPSLGGGGGCGALPVSGAAQWAPVLDFAAPGASAYGSLGGAPPAPP 191

QY 69 PPPPPPHSFIKQEPSWGGAEPEEQCLSAFTVHFSQGTGTAGACRYGPGPPPPSQAS 128
Db 192 PPPPPPHSFIKQEPSWGGAEPEEQCLSAFTVHFSQGTGTAGACRYGPGPPPPSQAS 251

QY 129 SGQARMPNAPYLPSCLESQPAIRNQGYSTVTFDGTPTSGHTPSHAAQPPNHSFKHEDP 188
Db 252 SGQARMPNAPYLPSCLESQPAIRNQGYSTVTFDGTPTSGHTPSHAAQPPNHSFKHEDP 311

QY 189 MGQGSIGEQQYVPPPPVYCHTPTDSCGQALLLRTPYSSDNLXQMTSOLCMTWNQM 248
Db 312 MGQGSIGEQQYVPPPPVYCHTPTDSCGQALLLRTPYSSDNLXQMTSOLCMTWNQM 371

QY 249 NLGATLKG 256
Db 372 NLGATLKG 379

RESULT 13
US-09-949-016-9406
; Sequence 9406, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9406
; LENGTH: 576
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-9406

Query Match 96.0%; Score 1386; DB 4; Length 576;
Best Local Similarity 100.0%; Pred. No. 1.9e-110;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GSDVRDLNALLPAVPSLGGGGGCGALPVSGAAQWAPVLDFAAPGASAYGSLGGAPPAPP 68
Db 132 GSDVRDLNALLPAVPSLGGGGGCGALPVSGAAQWAPVLDFAAPGASAYGSLGGAPPAPP 191

QY 69 PPPPPPHSFIKQEPSWGGAEPEEQCLSAFTVHFSQGTGTAGACRYGPGPPPPSQAS 128
Db 192 PPPPPPHSFIKQEPSWGGAEPEEQCLSAFTVHFSQGTGTAGACRYGPGPPPPSQAS 251

QY 129 SGQARMPNAPYLPSCLESQPAIRNQGYSTVTFDGTPTSGHTPSHAAQPPNHSFKHEDP 188
Db 252 SGQARMPNAPYLPSCLESQPAIRNQGYSTVTFDGTPTSGHTPSHAAQPPNHSFKHEDP 311

QY 189 MGQGSIGEQQYVPPPPVYCHTPTDSCGQALLLRTPYSSDNLXQMTSOLCMTWNQM 248
Db 312 MGQGSIGEQQYVPPPPVYCHTPTDSCGQALLLRTPYSSDNLXQMTSOLCMTWNQM 371

QY 249 NLGATLKG 256
Db 372 NLGATLKG 379

RESULT 14
US-09-949-016-9407
; Sequence 9407, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9407
; LENGTH: 576
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-9407

Query Match 96.0%; Score 1386; DB 4; Length 576;
Best Local Similarity 100.0%; Pred. No. 1.9e-110;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GSDVRDLNALLPAVPSLGGGGGCGALPVSGAAQWAPVLDFAAPGASAYGSLGGAPPAPP 68
Db 132 GSDVRDLNALLPAVPSLGGGGGCGALPVSGAAQWAPVLDFAAPGASAYGSLGGAPPAPP 191

QY 69 PPPPPPHSFIKQEPSWGGAEPEEQCLSAFTVHFSQGTGTAGACRYGPGPPPPSQAS 128
Db 192 PPPPPPHSFIKQEPSWGGAEPEEQCLSAFTVHFSQGTGTAGACRYGPGPPPPSQAS 251

QY 129 SGQARMPNAPYLPSCLESQPAIRNQGYSTVTFDGTPTSGHTPSHAAQPPNHSFKHEDP 188
Db 252 SGQARMPNAPYLPSCLESQPAIRNQGYSTVTFDGTPTSGHTPSHAAQPPNHSFKHEDP 311

QY 189 MGQGSIGEQQYVPPPPVYCHTPTDSCGQALLLRTPYSSDNLXQMTSOLCMTWNQM 248
Db 312 MGQGSIGEQQYVPPPPVYCHTPTDSCGQALLLRTPYSSDNLXQMTSOLCMTWNQM 371

QY 249 NLGATLKG 256
Db 372 NLGATLKG 379

```

```

; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9406
; LENGTH: 576
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-9406

Query Match 96.0%; Score 1386; DB 4; Length 576;
Best Local Similarity 100.0%; Pred. No. 1.9e-110;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GSDVRDLNALLPAVPSLGGGGGCGALPVSGAAQWAPVLDFAAPGASAYGSLGGAPPAPP 68
Db 132 GSDVRDLNALLPAVPSLGGGGGCGALPVSGAAQWAPVLDFAAPGASAYGSLGGAPPAPP 191

QY 69 PPPPPPHSFIKQEPSWGGAEPEEQCLSAFTVHFSQGTGTAGACRYGPGPPPPSQAS 128
Db 192 PPPPPPHSFIKQEPSWGGAEPEEQCLSAFTVHFSQGTGTAGACRYGPGPPPPSQAS 251

QY 129 SGQARMPNAPYLPSCLESQPAIRNQGYSTVTFDGTPTSGHTPSHAAQPPNHSFKHEDP 188
Db 252 SGQARMPNAPYLPSCLESQPAIRNQGYSTVTFDGTPTSGHTPSHAAQPPNHSFKHEDP 311

QY 189 MGQGSIGEQQYVPPPPVYCHTPTDSCGQALLLRTPYSSDNLXQMTSOLCMTWNQM 248
Db 312 MGQGSIGEQQYVPPPPVYCHTPTDSCGQALLLRTPYSSDNLXQMTSOLCMTWNQM 371

QY 249 NLGATLKG 256
Db 372 NLGATLKG 379

RESULT 14
US-09-949-016-9407
; Sequence 9407, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9407
; LENGTH: 576
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-9407

Query Match 96.0%; Score 1386; DB 4; Length 576;
Best Local Similarity 100.0%; Pred. No. 1.9e-110;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GSDVRDLNALLPAVPSLGGGGGCGALPVSGAAQWAPVLDFAAPGASAYGSLGGAPPAPP 68
Db 132 GSDVRDLNALLPAVPSLGGGGGCGALPVSGAAQWAPVLDFAAPGASAYGSLGGAPPAPP 191

QY 69 PPPPPPHSFIKQEPSWGGAEPEEQCLSAFTVHFSQGTGTAGACRYGPGPPPPSQAS 128
Db 192 PPPPPPHSFIKQEPSWGGAEPEEQCLSAFTVHFSQGTGTAGACRYGPGPPPPSQAS 251

QY 129 SGQARMPNAPYLPSCLESQPAIRNQGYSTVTFDGTPTSGHTPSHAAQPPNHSFKHEDP 188
Db 252 SGQARMPNAPYLPSCLESQPAIRNQGYSTVTFDGTPTSGHTPSHAAQPPNHSFKHEDP 311

QY 189 MGQGSIGEQQYVPPPPVYCHTPTDSCGQALLLRTPYSSDNLXQMTSOLCMTWNQM 248
Db 312 MGQGSIGEQQYVPPPPVYCHTPTDSCGQALLLRTPYSSDNLXQMTSOLCMTWNQM 371

QY 249 NLGATLKG 256
Db 372 NLGATLKG 379

```


Qy 129 SGOARMPNAPYLPSCLESQPAIRNQYSTVTFDGTSPSYGHTPSHHAAQFPNHSFKHEDP 188
Dy 252 SGOARMPNAPYLPSCLESQPAIRNQYSTVTFDGTSPSYGHTPSHHAAQFPNHSFKHEDP 311
Qy 189 MGQOGSLGEQOYSVPPPVYGGHTPTDCTGSOALLRLTPYSSDNLQYMTSOLSCMTWNQ 248
Dy 312 MGQOGSLGEQOYSVPPPVYGGHTPTDCTGSOALLRLTPYSSDNLQYMTSOLSCMTWNQ 371
Qy 249 NLGATLKG 256
Dy 372 NLGATLKG 379

RESULT 15

US-08-102-942A-4
; Sequence 4, Application US/08102942A
; Patent No. 5726288
; GENERAL INFORMATION:
; APPLICANT: Call, Katherine M.
; APPLICANT: Glaser, Thomas M.
; APPLICANT: Ito, Caryn Y.
; APPLICANT: Buckler, Alan J.
; APPLICANT: Pelletier, Jerry
; APPLICANT: Haber, Daniel A.
; APPLICANT: Rose, Elise A.
; APPLICANT: Housman, David E.
; APPLICANT: Bruening, Wendy
; APPLICANT: Darveau, Andre
; TITLE OF INVENTION: Localization and Characterization of the
; TITLE OF INVENTION: Wilms' Tumor Gene
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/102,942A
; FILING DATE: 02-AUG-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: MIT-5194A2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 449 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-102-942A-4

Query Match 92.0%; Score 1329; DB 1; Length 449;
Best Local Similarity 96.8%; Pred. No. 1e-105;
Matches 241; Conservative 1; Mismatches 5; Indels 2; Gaps 2;
Qy 9 GSDVRDLNALLPAYPSL-GGGGGGALPVSGAAQWAPVLDFAAPGASAYGSLGGPAPPAP 67
Dy 2 GSDVRDLNALLPAYVSSLGCGGGGGLPVSGARQWAPVLDFAAPGASAYGSLGGPAPPAP 60
Qy 68 PPPPPPPHPSFIKQEPSWGAEPHEEOCLSAFTVHFSQGTGTAGACRYGFGPPPPPSQA 127

Db 61 PPPPPPPHPSFIKQEPSWGAEPHEEOCLSAFTVHFSQGTGTAGACRYGFGPPPPPSQA 120
Qy 128 SSGQARMPNAPYLPSCLESQPAIRNQYSTVTFDGTSPSYGHTPSHHAAQFPNHSFKHED 187
Dy 121 SSGQARMPNAPYLPSCLESQPAIRNQYSTVTFDGTSPSYGHTPSHHAAQFPNHSFKHED 180
Qy 188 PMGQOGSLGEQOYSVPPPVYGGHTPTDCTGSOALLRLTPYSSDNLQYMTSOLSCMTWNQ 247
Dy 181 PMGQOGSLGEQOYSVPPPVYGGHTPTDCTGSOALLRLTPYSSDNLQYMTSOLSCMTWNQ 240
Qy 248 MNLGATLKG 256
Dy 241 MNLGATLKG 249

Search completed: May 10, 2005, 18:46:22
Job time : 45 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 10, 2005, 18:42:00 ; Search time 135 Seconds
(without alignments)
632.602 Million cell updates/sec

Title: US-09-785-019B-335
Perfect score: 1444
Sequence: 1 MQHHHHGSDVRLNALLP.....TSOLECTWQMNLGATLKG 256

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1428581 seqs, 333598853 residues

Total number of hits satisfying chosen parameters: 1428581

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				
Result No.	Score	Query Match	Length DB ID	Description
1	1444	100.0	256 10	US-09-938-864-335 Sequence 335, App
2	1444	100.0	256 10	US-09-785-019-335 Sequence 335, App
3	1444	100.0	256 14	US-10-125-635A-335 Sequence 335, App
4	1444	100.0	256 14	US-10-002-603-335 Sequence 335, App
5	1444	100.0	256 14	US-10-195-835-335 Sequence 335, App
6	1444	100.0	256 15	US-10-286-333-335 Sequence 335, App
7	1444	100.0	256 15	US-10-244-830-335 Sequence 335, App
8	1444	100.0	256 15	US-10-427-717-335 Sequence 335, App
9	1444	100.0	256 16	US-10-648-780-335 Sequence 335, App
10	1418.5	98.2	410 10	US-09-938-864-333 Sequence 333, App
11	1418.5	98.2	410 10	US-09-785-019-333 Sequence 333, App
12	1418.5	98.2	410 14	US-10-125-635A-333 Sequence 333, App
13	1418.5	98.2	410 14	US-10-002-603-333 Sequence 333, App

14	1418.5	98.2	410	14	US-10-195-835-333	Sequence 333, App
15	1418.5	98.2	410	15	US-10-286-333-333	Sequence 333, App
16	1418.5	98.2	410	16	US-10-244-830-333	Sequence 333, App
17	1418.5	98.2	410	17	US-10-427-717-333	Sequence 333, App
18	1418.5	98.2	410	18	US-10-648-780-333	Sequence 333, App
19	1418	98.2	591	19	US-09-938-864-334	Sequence 334, App
20	1418	98.2	591	20	US-09-785-019-334	Sequence 334, App
21	1418	98.2	591	21	US-10-125-635A-334	Sequence 334, App
22	1418	98.2	591	22	US-10-002-603-334	Sequence 334, App
23	1418	98.2	591	23	US-10-195-835-334	Sequence 334, App
24	1418	98.2	591	24	US-10-244-830-334	Sequence 334, App
25	1418	98.2	591	25	US-10-427-717-334	Sequence 334, App
26	1418	98.2	591	26	US-10-648-780-334	Sequence 334, App
27	1418	98.2	591	27	US-10-286-333-470	Sequence 470, App
28	1394	96.5	292	28	US-10-286-333-499	Sequence 499, App
29	1394	96.5	292	29	US-10-427-717-470	Sequence 470, App
30	1394	96.5	292	30	US-10-427-717-499	Sequence 499, App
31	1394	96.5	292	31	US-10-125-635A-455	Sequence 455, App
32	1394	96.5	321	32	US-10-195-835-455	Sequence 455, App
33	1394	96.5	321	33	US-10-286-333-455	Sequence 455, App
34	1394	96.5	321	34	US-10-286-333-479	Sequence 479, App
35	1394	96.5	321	35	US-10-244-830-455	Sequence 455, App
36	1394	96.5	321	36	US-10-427-717-455	Sequence 455, App
37	1394	96.5	321	37	US-10-427-717-479	Sequence 479, App
38	1394	96.5	321	38	US-10-648-780-455	Sequence 455, App
39	1394	96.5	321	39	US-10-125-635A-454	Sequence 454, App
40	1394	96.5	469	40	US-10-195-835-454	Sequence 454, App
41	1394	96.5	469	41	US-10-286-333-454	Sequence 454, App
42	1394	96.5	469	42	US-10-244-830-454	Sequence 454, App
43	1394	96.5	469	43	US-10-427-717-454	Sequence 454, App
44	1394	96.5	469	44	US-10-648-780-454	Sequence 454, App
45	1394	96.5	469	45	US-10-286-333-454	Sequence 454, App

ALIGNMENTS

RESULT 1

US-09-938-864-335
; Sequence 335, Application US/09938864
; Publication No. US2003007267A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Mossman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Spies, A. Gregory
; APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WTL
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
; FILE REFERENCE: 210121.465C5
; CURRENT APPLICATION NUMBER: US/09/938,864
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 335
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-938-864-335

Query Match 100.0%; Score 1444; DB 10; Length 256;
Best Local Similarity 100.0%; Pred. No. 1.8e-90;
Matches 256; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;
Qy 1 MQHHHHGSDVRLNALLPVPVSLGGGGGCAIPVSGAAQWAPVLDFAFGASAYSLGG 60
Db 1 MQHHHHGSDVRLNALLPVPVSLGGGGGCAIPVSGAAQWAPVLDFAFGASAYSLGG 60

Qy 61 PAPPAPPPPPPPPHSFQKQPSWGAEPHEEQCLSAFTVHFSQGTGTAGACRYGPF 120
Db 61 PAPPAPPPPPPPPHSFQKQPSWGAEPHEEQCLSAFTVHFSQGTGTAGACRYGPF 120
Qy 121 PPPSQASSQOARMFPNAPYLPSCLESQPAIRNQGYSVTFTDGTSPSYGHTPSHHAQFPN 180
Db 121 PPPSQASSQOARMFPNAPYLPSCLESQPAIRNQGYSVTFTDGTSPSYGHTPSHHAQFPN 180
Qy 181 HSPKHEDPMQOQSLGEOQSVPPPVYVGGTCTGSGQALLRTPTSSDNLQYMTSQL 240
Db 181 HSPKHEDPMQOQSLGEOQSVPPPVYVGGTCTGSGQALLRTPTSSDNLQYMTSQL 240
Qy 241 ECMTWQNMNLGATLKG 256
Db 241 ECMTWQNMNLGATLKG 256

RESULT 2

US-09-785-019-335
; Sequence 335, Application US/09785019
; Publication No. US20030082196A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE OF INVENTION: SPECIFIC IMMUNOTHERAPY
; FILE REFERENCE: 210121.465C4
; CURRENT APPLICATION NUMBER: US/09/785,019
; CURRENT FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 335
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-785-019-335

Query Match 100.0%; Score 1444; DB 10; Length 256;
Best Local Similarity 100.0%; Pred. No. 1.8e-90;
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MQHHHHHGSVDRLNALLPAVPSLGGGGGCGALPVSGAAQWAPVLDPAFPGASAYGSLGG 60
Db 1 MQHHHHHGSVDRLNALLPAVPSLGGGGGCGALPVSGAAQWAPVLDPAFPGASAYGSLGG 60
Qy 61 PAPPAPPPPPPPPHSFQKQPSWGAEPHEEQCLSAFTVHFSQGTGTAGACRYGPF 120
Db 61 PAPPAPPPPPPPPHSFQKQPSWGAEPHEEQCLSAFTVHFSQGTGTAGACRYGPF 120
Qy 121 PPPSQASSQOARMFPNAPYLPSCLESQPAIRNQGYSVTFTDGTSPSYGHTPSHHAQFPN 180
Db 121 PPPSQASSQOARMFPNAPYLPSCLESQPAIRNQGYSVTFTDGTSPSYGHTPSHHAQFPN 180
Qy 181 HSPKHEDPMQOQSLGEOQSVPPPVYVGGTCTGSGQALLRTPTSSDNLQYMTSQL 240
Db 181 HSPKHEDPMQOQSLGEOQSVPPPVYVGGTCTGSGQALLRTPTSSDNLQYMTSQL 240
Qy 241 ECMTWQNMNLGATLKG 256
Db 241 ECMTWQNMNLGATLKG 256

RESULT 3

US-10-125-635A-335
; Sequence 335, Application US/10125635A
; Publication No. US20030039635A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander

; APPLICANT: Smithgall, Molly D.
; APPLICANT: Carter, Darrick
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Sutherland, R. Alec.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE OF INVENTION: SPECIFIC IMMUNOTHERAPY
; FILE REFERENCE: 210121.465C7
; CURRENT APPLICATION NUMBER: US/10/125,635A
; CURRENT FILING DATE: 2002-07-19
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 335
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-125-635A-335

Query Match 100.0%; Score 1444; DB 14; Length 256;
Best Local Similarity 100.0%; Pred. No. 1.8e-90;
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MQHHHHHGSVDRLNALLPAVPSLGGGGGCGALPVSGAAQWAPVLDPAFPGASAYGSLGG 60
Db 1 MQHHHHHGSVDRLNALLPAVPSLGGGGGCGALPVSGAAQWAPVLDPAFPGASAYGSLGG 60
Qy 61 PAPPAPPPPPPPPHSFQKQPSWGAEPHEEQCLSAFTVHFSQGTGTAGACRYGPF 120
Db 61 PAPPAPPPPPPPPHSFQKQPSWGAEPHEEQCLSAFTVHFSQGTGTAGACRYGPF 120
Qy 121 PPPSQASSQOARMFPNAPYLPSCLESQPAIRNQGYSVTFTDGTSPSYGHTPSHHAQFPN 180
Db 121 PPPSQASSQOARMFPNAPYLPSCLESQPAIRNQGYSVTFTDGTSPSYGHTPSHHAQFPN 180
Qy 181 HSPKHEDPMQOQSLGEOQSVPPPVYVGGTCTGSGQALLRTPTSSDNLQYMTSQL 240
Db 181 HSPKHEDPMQOQSLGEOQSVPPPVYVGGTCTGSGQALLRTPTSSDNLQYMTSQL 240
Qy 241 ECMTWQNMNLGATLKG 256
Db 241 ECMTWQNMNLGATLKG 256

RESULT 4

US-10-002-603-335
; Sequence 335, Application US/10002603
; Publication No. US2003005971A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Mossman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Spies, A. Gregory
; APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE OF INVENTION: SPECIFIC IMMUNOTHERAPY
; FILE REFERENCE: 210121.465C6
; CURRENT APPLICATION NUMBER: US/10/002,603
; CURRENT FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 335
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-002-603-335

Query Match 100.0%; Score 1444; DB 14; Length 256;
Best Local Similarity 100.0%; Pred. No. 1.8e-90;


```
Db 1 MQHHHHGSDVRLNALLPAVPSLGGGGCALPVSGAAQWAPVLDFAPPGASAYSLGG 60
Qy 61 PAPPAPPPPPPPPHSFIKQEPSWGGAEPHEQCCLSAFTVHFSGQFTGTAGACRYGPPG 120
Db 61 PAPPAPPPPPPPPHSFIKQEPSWGGAEPHEQCCLSAFTVHFSGQFTGTAGACRYGPPG 120
Qy 121 PPPSQASSQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTSPSYGHTPSHHAQFPN 180
Db 121 PPPSQASSQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTSPSYGHTPSHHAQFPN 180
Qy 181 HSFKHEDPMQOQSLGEGQYVPPPVYGGCHTPTDCTGSQLLLRTPYSSDNLQYMTSQL 240
Db 181 HSFKHEDPMQOQSLGEGQYVPPPVYGGCHTPTDCTGSQLLLRTPYSSDNLQYMTSQL 240
Qy 241 ECMTWQNMNLGATLKG 256
Db 241 ECMTWQNMNLGATLKG 256

RESULT 8
US-10-427-717-335
; Sequence 335, Application US/10427717
; Publication No. US20040018204A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
; FILE REFERENCE: 210121.465C11
; CURRENT APPLICATION NUMBER: US/10/427,717
; CURRENT FILING DATE: 2003-04-30
; NUMBER OF SEQ ID NOS: 508
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 335
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-427-717-335

Query Match 100.0%; Score 1444; DB 15; Length 256;
Best Local Similarity 100.0%; Pred. No. 1.8e-90;
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQHHHHGSDVRLNALLPAVPSLGGGGCALPVSGAAQWAPVLDFAPPGASAYSLGG 60
Db 1 MQHHHHGSDVRLNALLPAVPSLGGGGCALPVSGAAQWAPVLDFAPPGASAYSLGG 60
Qy 61 PAPPAPPPPPPPPHSFIKQEPSWGGAEPHEQCCLSAFTVHFSGQFTGTAGACRYGPPG 120
Db 61 PAPPAPPPPPPPPHSFIKQEPSWGGAEPHEQCCLSAFTVHFSGQFTGTAGACRYGPPG 120
Qy 121 PPPSQASSQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTSPSYGHTPSHHAQFPN 180
Db 121 PPPSQASSQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTSPSYGHTPSHHAQFPN 180
Qy 181 HSFKHEDPMQOQSLGEGQYVPPPVYGGCHTPTDCTGSQLLLRTPYSSDNLQYMTSQL 240
Db 181 HSFKHEDPMQOQSLGEGQYVPPPVYGGCHTPTDCTGSQLLLRTPYSSDNLQYMTSQL 240
Qy 241 ECMTWQNMNLGATLKG 256
Db 241 ECMTWQNMNLGATLKG 256

RESULT 9
US-10-648-780-335
; Sequence 335, Application US/10648780
; Publication No. US20040126362A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Smithgall, Molly D.
US-10-648-780-335

Query Match 100.0%; Score 1444; DB 15; Length 256;
Best Local Similarity 100.0%; Pred. No. 1.8e-90;
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQHHHHGSDVRLNALLPAVPSLGGGGCALPVSGAAQWAPVLDFAPPGASAYSLGG 60
Db 1 MQHHHHGSDVRLNALLPAVPSLGGGGCALPVSGAAQWAPVLDFAPPGASAYSLGG 60
Qy 61 PAPPAPPPPPPPPHSFIKQEPSWGGAEPHEQCCLSAFTVHFSGQFTGTAGACRYGPPG 120
Db 61 PAPPAPPPPPPPPHSFIKQEPSWGGAEPHEQCCLSAFTVHFSGQFTGTAGACRYGPPG 120
Qy 121 PPPSQASSQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTSPSYGHTPSHHAQFPN 180
Db 121 PPPSQASSQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTSPSYGHTPSHHAQFPN 180
Qy 181 HSFKHEDPMQOQSLGEGQYVPPPVYGGCHTPTDCTGSQLLLRTPYSSDNLQYMTSQL 240
Db 181 HSFKHEDPMQOQSLGEGQYVPPPVYGGCHTPTDCTGSQLLLRTPYSSDNLQYMTSQL 240
Qy 241 ECMTWQNMNLGATLKG 256
Db 241 ECMTWQNMNLGATLKG 256

RESULT 10
US-09-938-864-333
; Sequence 333, Application US/09938864
; Publication No. US20030072767A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Mossman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Spies, A. Gregory
; APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
; FILE REFERENCE: 210121.465C5
; CURRENT APPLICATION NUMBER: US/09/938,864
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 333
; LENGTH: 410
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-938-864-333

Query Match 100.0%; Score 1444; DB 16; Length 256;
Best Local Similarity 100.0%; Pred. No. 1.8e-90;
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQHHHHGSDVRLNALLPAVPSLGGGGCALPVSGAAQWAPVLDFAPPGASAYSLGG 60
Db 1 MQHHHHGSDVRLNALLPAVPSLGGGGCALPVSGAAQWAPVLDFAPPGASAYSLGG 60
Qy 61 PAPPAPPPPPPPPHSFIKQEPSWGGAEPHEQCCLSAFTVHFSGQFTGTAGACRYGPPG 120
Db 61 PAPPAPPPPPPPPHSFIKQEPSWGGAEPHEQCCLSAFTVHFSGQFTGTAGACRYGPPG 120
Qy 121 PPPSQASSQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTSPSYGHTPSHHAQFPN 180
Db 121 PPPSQASSQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTSPSYGHTPSHHAQFPN 180
Qy 181 HSFKHEDPMQOQSLGEGQYVPPPVYGGCHTPTDCTGSQLLLRTPYSSDNLQYMTSQL 240
Db 181 HSFKHEDPMQOQSLGEGQYVPPPVYGGCHTPTDCTGSQLLLRTPYSSDNLQYMTSQL 240
Qy 241 ECMTWQNMNLGATLKG 256
Db 241 ECMTWQNMNLGATLKG 256
```

Query Match 98.2%; Score 1418.5; DB 10; Length 410;
Best Local Similarity 89.2%; Pred. No. 1.5e-88;
Matches 256; Conservative 0; Mismatches 0; Indels 31; Gaps 1;

QY 1 MQHHHHH-----GSDVRDLNALLPAVPSLGGG 29
| | | | |
Db 124 MQHHHHHVSIIEGRASSGSLVPRGSSGDDDDKSSRGSDVRDLNALLPAVPSLGGG 183
| | | | |
QY 30 GCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPPPPPPHSHFKQEPSWGAE 89
| | | | |
Db 184 GCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPPPPPPHSHFKQEPSWGAE 243
| | | | |
QY 90 PHEEQCLSAFTVHFSGQFTGTAGACRYGPFPPPPPSQASSGQARMFPNAPVLPSCLESQP 149
| | | | |
Db 244 PHEEQCLSAFTVHFSGQFTGTAGACRYGPFPPPPPSQASSGQARMFPNAPVLPSCLESQP 303
| | | | |
QY 150 AIRNQGYSTVTFDGTPTSGYHTPSHAAQFPNHSFKHEDPMGQGSGLGEQQYVPPPYGC 209
| | | | |
Db 304 AIRNQGYSTVTFDGTPTSGYHTPSHAAQFPNHSFKHEDPMGQGSGLGEQQYVPPPYGC 363
| | | | |
QY 210 HTPTDCTGSOALLRTPYSSDNLQYMTSOLECMTWQNMNGLATLKG 256
| | | | |
Db 364 HTPTDCTGSOALLRTPYSSDNLQYMTSOLECMTWQNMNGLATLKG 410
| | | | |

RESULT 11
US-09-785-019-333
; Sequence 333, Application US/09785019
; Publication No. US20030082196A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
; FILE REFERENCE: 210121.465C4
; CURRENT APPLICATION NUMBER: US/09/785,019
; CURRENT FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 333
; LENGTH: 410
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-785-019-333

Query Match 98.2%; Score 1418.5; DB 10; Length 410;
Best Local Similarity 89.2%; Pred. No. 1.5e-88;
Matches 256; Conservative 0; Mismatches 0; Indels 31; Gaps 1;

QY 1 MQHHHHH-----GSDVRDLNALLPAVPSLGGG 29
| | | | |
Db 124 MQHHHHHVSIIEGRASSGSLVPRGSSGDDDDKSSRGSDVRDLNALLPAVPSLGGG 183
| | | | |
QY 30 GCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPPPPPPHSHFKQEPSWGAE 89
| | | | |
Db 184 GCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPPPPPPHSHFKQEPSWGAE 243
| | | | |
QY 90 PHEEQCLSAFTVHFSGQFTGTAGACRYGPFPPPPPSQASSGQARMFPNAPVLPSCLESQP 149
| | | | |
Db 244 PHEEQCLSAFTVHFSGQFTGTAGACRYGPFPPPPPSQASSGQARMFPNAPVLPSCLESQP 303
| | | | |
QY 150 AIRNQGYSTVTFDGTPTSGYHTPSHAAQFPNHSFKHEDPMGQGSGLGEQQYVPPPYGC 209
| | | | |
Db 304 AIRNQGYSTVTFDGTPTSGYHTPSHAAQFPNHSFKHEDPMGQGSGLGEQQYVPPPYGC 363
| | | | |
QY 210 HTPTDCTGSOALLRTPYSSDNLQYMTSOLECMTWQNMNGLATLKG 256
| | | | |
Db 364 HTPTDCTGSOALLRTPYSSDNLQYMTSOLECMTWQNMNGLATLKG 410
| | | | |

RESULT 12
US-10-125-635A-333
; Sequence 333, Application US/10125635A
; Publication No. US20030039635A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Smithgall, Molly D.
; APPLICANT: Carter, Darrick
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Sucherland, R. Alec
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
; FILE REFERENCE: 210121.465C7
; CURRENT APPLICATION NUMBER: US/10/125,635A
; CURRENT FILING DATE: 2002-07-19
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 333
; LENGTH: 410
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-125-635A-333

Query Match 98.2%; Score 1418.5; DB 14; Length 410;
Best Local Similarity 89.2%; Pred. No. 1.5e-88;
Matches 256; Conservative 0; Mismatches 0; Indels 31; Gaps 1;

QY 1 MQHHHHH-----GSDVRDLNALLPAVPSLGGG 29
| | | | |
Db 124 MQHHHHHVSIIEGRASSGSLVPRGSSGDDDDKSSRGSDVRDLNALLPAVPSLGGG 183
| | | | |
QY 30 GCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPPPPPPHSHFKQEPSWGAE 89
| | | | |
Db 184 GCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPPPPPPHSHFKQEPSWGAE 243
| | | | |
QY 90 PHEEQCLSAFTVHFSGQFTGTAGACRYGPFPPPPPSQASSGQARMFPNAPVLPSCLESQP 149
| | | | |
Db 244 PHEEQCLSAFTVHFSGQFTGTAGACRYGPFPPPPPSQASSGQARMFPNAPVLPSCLESQP 303
| | | | |
QY 150 AIRNQGYSTVTFDGTPTSGYHTPSHAAQFPNHSFKHEDPMGQGSGLGEQQYVPPPYGC 209
| | | | |
Db 304 AIRNQGYSTVTFDGTPTSGYHTPSHAAQFPNHSFKHEDPMGQGSGLGEQQYVPPPYGC 363
| | | | |
QY 210 HTPTDCTGSOALLRTPYSSDNLQYMTSOLECMTWQNMNGLATLKG 256
| | | | |
Db 364 HTPTDCTGSOALLRTPYSSDNLQYMTSOLECMTWQNMNGLATLKG 410
| | | | |

RESULT 13
US-10-002-603-333
; Sequence 333, Application US/10002603
; Publication No. US20030095971A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Mossman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Spies, A. Gregory
; APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
; FILE REFERENCE: 210121.465C6
; CURRENT APPLICATION NUMBER: US/10/002,603
; CURRENT FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSeq for Windows Version 3.0

```
; SEQ ID NO 333
; LENGTH: 410
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-002-603-333

Query Match      98.2%; Score 1418.5; DB 14; Length 410;
Best Local Similarity 89.2%; Pred. No. 1.5e-88;
Matches 256; Conservative 0; Mismatches 0; Indels 31; Gaps 1;

QY 1 MQHHHHH-----GSDVRDLNALLPAVPSLGGGG 29
Db 124 MQHHHHHVSIEGRASSGSGLVPRGSGSGDDDDKSSRGSDVRDLNALLPAVPSLGGGG 183
QY 30 GCALPVSGAAQWAPVLDFAFPGASAYGSLGGPAPPPPPPHSF1KQEPSWGAE 89
Db 184 GCALPVSGAAQWAPVLDFAFPGASAYGSLGGPAPPPPPPHSF1KQEPSWGAE 243
QY 90 PHEEQCLSAFTVHFSGQFTGTAGACRYGPGFPFPPPSQASSGQARMFNAPYLPSCLESQP 149
Db 244 PHEEQCLSAFTVHFSGQFTGTAGACRYGPGFPFPPPSQASSGQARMFNAPYLPSCLESQP 303
QY 150 AIRNOGYSTVTFDGTPTSYGHTPSHHAQFPNHSFKHEDPMGQGSGLGEQOQYSVPPPVYGC 209
Db 304 AIRNOGYSTVTFDGTPTSYGHTPSHHAQFPNHSFKHEDPMGQGSGLGEQOQYSVPPPVYGC 363
QY 210 HTPDSDCTGSOALLLRTPTPYSSDNLQYMTSOLECMTWNQMNLGATLKG 256
Db 364 HTPDSDCTGSOALLLRTPTPYSSDNLQYMTSOLECMTWNQMNLGATLKG 410

RESULT 15
US-10-286-333-333
; Sequence 333, Application US/10286333
; Publication No. US20030215458A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Jaya, No. US20030215458A1a1a1e
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
; FILE REFERENCE: 210121.465C10
; CURRENT APPLICATION NUMBER: US/10/286,333
; CURRENT FILING DATE: 2002-10-30
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 333
; LENGTH: 410
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-286-333-333

Query Match      98.2%; Score 1418.5; DB 15; Length 410;
Best Local Similarity 89.2%; Pred. No. 1.5e-88;
Matches 256; Conservative 0; Mismatches 0; Indels 31; Gaps 1;

QY 1 MQHHHHH-----GSDVRDLNALLPAVPSLGGGG 29
Db 124 MQHHHHHVSIEGRASSGSGLVPRGSGSGDDDDKSSRGSDVRDLNALLPAVPSLGGGG 183
QY 30 GCALPVSGAAQWAPVLDFAFPGASAYGSLGGPAPPPPPPHSF1KQEPSWGAE 89
Db 184 GCALPVSGAAQWAPVLDFAFPGASAYGSLGGPAPPPPPPHSF1KQEPSWGAE 243
QY 90 PHEEQCLSAFTVHFSGQFTGTAGACRYGPGFPFPPPSQASSGQARMFNAPYLPSCLESQP 149
Db 244 PHEEQCLSAFTVHFSGQFTGTAGACRYGPGFPFPPPSQASSGQARMFNAPYLPSCLESQP 303
QY 150 AIRNOGYSTVTFDGTPTSYGHTPSHHAQFPNHSFKHEDPMGQGSGLGEQOQYSVPPPVYGC 209
Db 304 AIRNOGYSTVTFDGTPTSYGHTPSHHAQFPNHSFKHEDPMGQGSGLGEQOQYSVPPPVYGC 363
QY 210 HTPDSDCTGSOALLLRTPTPYSSDNLQYMTSOLECMTWNQMNLGATLKG 256
Db 364 HTPDSDCTGSOALLLRTPTPYSSDNLQYMTSOLECMTWNQMNLGATLKG 410

Search completed: May 10, 2005, 18:56:54
Job time : 136 secs
```


GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 10, 2005, 18:35:45 ; Search time 39 Seconds
(without alignments)
631.577 Million cell updates/sec

Title: US-09-785-019B-335
Perfect score: 1444
Sequence: 1 MQHHHHGSDVRDLNALLP.....TSQLECMWNQMLGATLKG 256

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79: *
1: piri: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1386	96.0	449	2 A38080	Wilms tumor suscep
2	1340.5	92.8	448	2 S33926	Wilms' tumor prote
3	1329	92.0	449	2 A39592	Wilms' tumor prote
4	971.5	67.3	410	2 JC5046	Wilms' tumor suppr
5	161.5	11.2	2715	2 T13049	eyelid - fruit fly
6	159.5	11.0	1585	2 T31611	hypothetical prote
7	148.5	10.3	530	2 A45690	transactivator EBN
8	145.5	10.1	576	2 T36729	probable serine/th
9	143	9.9	1176	2 T49482	hypothetical prote
10	142.5	9.9	1201	2 G86441	unknown protein [i
11	142	9.8	903	2 T00074	hypothetical prote
12	141	9.8	1018	2 T43168	hypothetical prote
13	141	9.8	1259	2 T16038	hypothetical prote
14	141	9.8	1541	2 T02831	AAA protein L4171.
15	140.5	9.7	1357	2 T29285	hypothetical prote
16	140	9.7	1132	2 A35098	MHC class III hist
17	139	9.6	530	2 T48627	hypothetical prote
18	139	9.6	990	2 T14756	hypothetical prote
19	138	9.6	172	2 D41132	collagen-related p
20	137.5	9.5	1443	2 S05979	steroid hormone re
21	137	9.5	306	2 T09067	extensin-like prot
22	136.5	9.5	1048	2 T31425	C-terminal domain
23	135.5	9.4	632	2 T02627	hypothetical prote
24	135	9.3	707	2 A46302	PTB-associated spl
25	135	9.3	1091	2 T13170	diaphanous protein
26	134.5	9.3	495	1 S31223	transcription fact
27	134	9.3	1184	2 G01763	atrophin-1 - human
28	133	9.2	684	2 A56154	Abi substrate ena
29	132	9.1	907	2 E96636	hypothetical prote

RESULT 1

A38080

Wilms tumor susceptibility protein Wt1 - human

C;Species: Homo sapiens (man)

C;Date: 31-Dec-1993 #sequence, revision 31-Dec-1993 #text, change 20-Jun-2000

C;Accession: A38080; S08273; A34673; I38504; I52811; I58315; A56411; S26286

R;Gessler, M.; Konig, A.; Bruns, G.A.

Genomics 12, 807-813, 1992

A;Title: The genomic organization and expression of the Wt1 gene.

A;Reference number: A38080; MUID:92241883; PMID:1572653

A;Accession: A38080

A;Molecule type: DNA

A;Residues: 1-449 <GES1>

A;Cross-references: GB:X61631; GB:S99414; NID:G37981; PIDN:CAA43819.1; PID:G825731

A;Note: it is uncertain whether Met-1 is the initiator or whether translation is initiated

A;Note: sequence extracted from NCBI backbone (NCBIN:99414, NCBIN:99422, NCBIN:99479, NC

A;Note: the sequence in GenBank entry HSWTGEX1, release 113.0, PIDN:CAA43819.1 differs i

R;Gessler, M.; Poustka, A.; Cavenee, W.; Neve, R.L.; Orkin, S.H.; Bruns, G.A.P.

Nature 343, 774-778, 1990

A;Title: Homozygous deletion in Wilms tumours of a zinc-finger gene identified by chromo

A;Reference number: S08273; MUID:90158822; PMID:2154702

A;Accession: S08273

A;Molecule type: mRNA

A;Residues: 'SRQPHGALRNPTACLPHPSPSLPPTHPRAGTAQAQPRLLAAILDFLLQLDPASTCVPEPASQHTI

A;Cross-references: EMBL:X51630; NID:G37977; PIDN:CAA35956.1; PID:G37978

R;Call, K.M.; Glaser, T.; Ito, C.Y.; Buckler, A.J.; Pelletier, J.; Haber, D.A.; Rose, E.

Cell 60, 509-520, 1990

A;Title: Isolation and characterization of a zinc finger polypeptide gene at the human cl

A;Reference number: A34673; MUID:90150277; PMID:2154335

A;Accession: A34673

A;Molecule type: mRNA

A;Residues: 85-249,267-364,'F',366-386,'T',388-407,411-449 <CAL>

A;Cross-references: GB:M30393; NID:G340381; PIDN:AAA36810.1; PID:G340382

R;Haber, D.A.; Sohn, R.L.; Buckler, A.J.; Pelletier, J.; Call, K.M.; Housman, D.E.

Proc. Natl. Acad. Sci. U.S.A. 88, 9618-9622, 1991

A;Title: Alternative splicing and genomic structure of the Wilms tumor gene Wt1.

A;Reference number: A56411; MUID:92052142; PMID:1658787

A;Contents: annotation; alternative splicing

R;Phelan, S.A.; Lindberg, C.; Call, K.M.

Cell Growth Differ. 5, 677-686, 1994

A;Title: Wilms' tumor gene, Wt1, mRNA is down-regulated during induction of erythroid an

A;Reference number: I38504; MUID:94368704; PMID:8086342

A;Accession: I38504

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-18 <PHE>

A;Cross-references: EMBL:U06486; NID:G473563; PIDN:AAA62865.1; PID:G458432

R;Pelletier, J.; Bruening, W.; Kashtan, C.E.; Maurer, S.M.; Manivel, J.C.; Striegel, J.E.

Cell 67, 437-447, 1991

A;Title: Germine mutations in the Wilms' tumor suppressor gene are associated with abno

A;Reference number: I52811; MUID:92005721; PMID:1655284

A;Accession: I52811

A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 355-365, 'H', 367-377 <PEL>
A;Cross-references: GB:S61513; NID:G237599; PIDN:AAB20109.1; PID:G237600
A;Note: mutant form
R;Hamilton, T.B.; Barilla, K.C.; Romaniuk, P.J.
Nucleic Acids Res. 23, 277-284, 1995
A;Title: High affinity binding sites for the Wilms' tumour suppressor protein WTI.
A;Reference number: I58315; MUID:95166649; PMID:7862533
A;Accession: I58315
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 'MGHHHHHHHSGHTEGRHM', 301-364, 'F', 366-386, 'T', 388-407, 411-449 <HAM>
A;Cross-references: GB:S75264; NID:G996246; PIDN:AAB33443.1; PID:G996247
A;Note: this sequence is engineered
C;Genetics:
A;Gene: GDB:WT1
A;Cross-references: GDB:I20496; OMIM:194070
A;Map position: 11p13-11p13
A;Introns: 148/1; 189/1; 223/2; 249/2; 266/2; 298/3; 349/1; 379/1; 410/1
A;Note: mRNA transcripts containing both alternatively spliced regions are the most abundant
C;Keywords: alternative splicing; DNA binding; kidney; tumor suppressor; zinc finger
F;1-449/Product: Wilms tumor susceptibility protein WTI, splice form 1 #status F
F;1-407,411-449/Product: Wilms tumor susceptibility protein WTI, splice form 4 #status F
F;1-249,267-449/Product: Wilms tumor susceptibility protein WTI, splice form 3 #status F
F;1-249,267-407,411-449/Product: Wilms tumor susceptibility protein WTI, splice form 2 #status F

Query Match 96.0%; Score 1386; DB 2; Length 449;
Best Local Similarity 100.0%; Pred. No. 1.5e-84;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GSDVRDLNALLPAVPSLGGGGGCGALPVSGAAQWAPVLDFAAPPASAYGSLGGPAPPAP 68
DB 2 GSDVRDLNALLPAVPSLGGGGGCGALPVSGAAQWAPVLDFAAPPASAYGSLGGPAPPAP 61
QY 69 PPPPPPHSFYIKQEPSWGAEPHEEQCLSAFTVHFSQQTGTAGACRYGFGPPPPSQAS 128
DB 62 PPPPPPHSFYIKQEPSWGAEPHEEQCLSAFTVHFSQQTGTAGACRYGFGPPPPSQAS 121
QY 129 SGQARMPNAPYLPSCLESQPAIRNQGYSYTVFDGTPSYGHTPSHHAQFPNHSFKHEDP 198
DB 122 SGQARMPNAPYLPSCLESQPAIRNQGYSYTVFDGTPSYGHTPSHHAQFPNHSFKHEDP 181
QY 189 MGQSGSLGEGQQYSVPPVYVGGCHTPTDCTGSQLLLRTPYSSDNLVYQMTSQLECMWTNQ 248
DB 182 MGQSGSLGEGQQYSVPPVYVGGCHTPTDCTGSQLLLRTPYSSDNLVYQMTSQLECMWTNQ 241
QY 249 NLGATLKG 256
DB 242 NLGATLKG 249

RESULT 2
S33926
Wilms' tumor protein WTI - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 10-May-1996
C;Accession: S33926
R;Sharma, P.M.; Yang, X.; Bowman, M.; Roberts, V.; Sukumar, S.
Cancer Res. 52, 6407-6412, 1992
A;Title: Molecular cloning of rat Wilms' tumor complementary DNA and a study of messenger RNA expression
A;Reference number: S33926; MUID:93046155; PMID:1330293
A;Accession: S33926
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-448 <SHA>
A;Cross-references: EMBL:X69716
C;Genetics:
A;Gene: WTI
C;Keywords: tumor suppressor

Query Match 92.8%; Score 1340.5; DB 2; Length 448;
Best Local Similarity 97.2%; Pred. No. 1.5e-81;

Matches 241; Conservative 2; Mismatches 4; Indels 1; Gaps 1;
QY 9 GSDVRDLNALLPAVPSLGGGGGCGALPVSGAAQWAPVLDFAAPPASAYGSLGGPAPPAP 68
DB 2 GSDVRDLNALLPAVPSLGGGGGCGALPVSGAAQWAPVLDFAAPPASAYGSLGGPAPPAP 60
QY 69 PPPPPPHSFYIKQEPSWGAEPHEEQCLSAFTVHFSQQTGTAGACRYGFGPPPPSQAS 128
DB 61 PPPPPPHSFYIKQEPSWGAEPHEEQCLSAFTVHFSQQTGTAGACRYGFGPPPPSQAS 120
QY 129 SGQARMPNAPYLPSCLESQPAIRNQGYSYTVFDGTPSYGHTPSHHAQFPNHSFKHEDP 198
DB 121 SGQARMPNAPYLPSCLESQPAIRNQGYSYTVFDGTPSYGHTPSHHAQFPNHSFKHEDP 180
QY 189 MGQSGSLGEGQQYSVPPVYVGGCHTPTDCTGSQLLLRTPYSSDNLVYQMTSQLECMWTNQ 248
DB 181 MGQSGSLGEGQQYSVPPVYVGGCHTPTDCTGSQLLLRTPYSSDNLVYQMTSQLECMWTNQ 240
QY 249 NLGATLKG 256
DB 241 NLGATLKG 248

RESULT 3
A39692
Wilms' tumor protein analog, WTI - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 16-Feb-1997
C;Accession: A39692
R;Buckler, A.J.; Pelletier, J.; Haber, D.A.; Glaser, T.; Hausman, D.E.
Mol. Cell. Biol. 11, 1707-1712, 1991
A;Title: Isolation, characterization, and expression of the murine Wilms' tumor gene (WT1)
A;Reference number: A39692; MUID:91141522; PMID:1671709
A;Accession: A39692
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-449 <BUC>
A;Cross-references: GB:M55512
C;Keywords: alternative splicing; DNA binding; transcription regulation; tumor suppressor

Query Match 92.0%; Score 1329; DB 2; Length 449;
Best Local Similarity 96.8%; Pred. No. 8.7e-81;
Matches 241; Conservative 1; Mismatches 5; Indels 2; Gaps 2;

QY 9 GSDVRDLNALLPAVPSLGGGGGCGALPVSGAAQWAPVLDFAAPPASAYGSLGGPAPPAP 67
DB 2 GSDVRDLNALLPAVPSLGGGGGCGALPVSGAAQWAPVLDFAAPPASAYGSLGGPAPPAP 60
QY 68 PPPPPPHSFYIKQEPSWGAEPHEEQCLSAFTVHFSQQTGTAGACRYGFGPPPPSQ 127
DB 61 PPPPPPHSFYIKQEPSWGAEPHEEQCLSAFTVHFSQQTGTAGACRYGFGPPPPSQ 120
QY 128 SSQARMPNAPYLPSCLESQPAIRNQGYSYTVFDGTPSYGHTPSHHAQFPNHSFKHED 187
DB 121 SSQARMPNAPYLPSCLESQPAIRNQGYSYTVFDGTPSYGHTPSHHAQFPNHSFKHED 180
QY 188 PMQOQSLGEGQQYSVPPVYVGGCHTPTDCTGSQLLLRTPYSSDNLVYQMTSQLECMWTNQ 247
DB 181 PMQOQSLGEGQQYSVPPVYVGGCHTPTDCTGSQLLLRTPYSSDNLVYQMTSQLECMWTNQ 240
QY 248 MNLGATLKG 256
DB 241 MNLGATLKG 249

RESULT 4
JC5046
Wilms' tumor suppressor protein - African clawed frog
N;Alternate names: WTI
C;Species: Xenopus laevis (African clawed frog)
C;Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 09-Jul-2004
C;Accession: JC5046
R;Semba, K.; Saito-Ueno, R.; Takayama, G.; Kondo, M.

[illegible]

RESULT 14
T02831
AAA protein L4171.3 [imported] - Leishmania major (strain Friedlin)
C:Species: Leishmania major
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C:Accession: C81460; T02831
P:Myler, P.J.; Audleman, L.; DeVos, T.; Hixson, G.; Kiser, P.; Lemley, C.; Mag
Proc. Natl. Acad. Sci. U.S.A. 96, 2902-2906, 1999
A:Title: Leishmania major Friedlin chromosome 1 has an unusual distribution of
A:Reference number: C81455; MUID:99178987; PMID:10077609
A:Accession: C81460
A:Status: preliminary
A:Residue type: DNA
A:Molecule type: DNA
A:Residues: 1-1541 <PVL>
A:Cross-references: UNIPROT:O15937; GB:AE001274; NID:G3264850; PIDN:AAC24654.1
A:Experimental source: strain MHOM/IL/81/Friedlin
C:Genetics:
A:Gene: L4171.3
A:Map position: 1

```

Query Match      9.8%; Score 141; DB 2; Length 1541;
Best Local Similarity 26.8%; Pred.No. 0.076;
Matches 61; Conservative 14; Mismatches 105; Indels 48; Gaps 10

Qy 27 GGGCGCALPVSQAQWAPVLDF-----PPGASAYG-- 56
      ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 90 GTCTGSGPASGAQTLLAPQAQSGAGKSMMPMPPEPMAGMVGMPMPMPGAAGSTGGM 149
      ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```
Qy 57 -SLGGPAPPAPPPPPPP---PPPHSFIKQSPSWGAGPHEEQCLSAFT--VHFSGGQFTGT 110
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
150 MSAGFMPPPPPPPPPPPPPPPLNGMIFQPPGTGMPHHHHHPAGMATPQCHLASQHQHQ 209
Qy 111 AGACRYGFPFPSPSQASSQAR----MFDNAPYLPSCLESQPAIRNQGYSTVTF-DGTP 165
Db   : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
210 HQHGMPMPMPMPPTQTQQHQQQQPGMMPMNSMMPM---SMFMSMPMGAASSLPLPGQH 266
Qy 166 SYGHTPSGHAAQFPNHSFK-HEDPMGQGSLSGEQQYSVPPPVYGYCHTP 212
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
267 SSG--PQOHPPQQPGMMMPFYPPQAPHGTM-PPWASMPPPAPCGMGPV 311
```

```
RESULT 15
T29265
hypothetical protein C01G8.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T29265
R;Du, Z.; Gattung, S.
submitted to the EMBL Data Library, November 1996
A;Description: The sequence of C. elegans cosmid C01G8.
A;Reference number: 220597
A;Accession: T29285
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1357 <DUZ>
A;Cross-references: EMBL:U80439; PIDN:AAB37645.1; GSPDB:GN00019; CESP:C01G8.7
A;Experimental source: strain Bristol N2; clone C01G8
C;Genetics:
A;Gene: CESP:C01G8.7
A;Map position: 1
A;Introns: 89/1; 488/1; 701/3; 1056/2; 1159/3; 1197/1; 1312/3
```

```
Query Match          9.7%; Score 140.5; DB 2; Length 1357;
Best Local Similarity 22.3%; Pred. No. 0.073;
Matches 62; Conservative 17; Mismatches 72; Indels 127; Gaps 14;

Qy 20 PAVPSLGGGGCALPVSGAAQWAPVLDFAFPASAY----- 55
Db 364 FGYPGYGPPGAMRPPAG-----FAPPPGAPYGPAGPPAGFPFHPQHPQHAQ 413
Qy 56 -----GSLGGPAPP-----PAPPPPP-----PPPHSFIKQEPS 84
Db 414 YLAWQQQRYHQOQHQOQOQOQOQAGPQGPYPYPYPGFVPGPQNRMPPPP-----PA 466
Qy 85 WGGAPHEEQCLSAFTVHFSQFTGTAGA---CRYGFPFPSPSQASSQAR-MFDNAP 139
Db 467 QGAPSP-----SGAAGSNGKQPRYGT--PAPPSRASATPQLSSTMP 507
Qy 140 YLPSCLESQPAIRNQGYSTVTFDGTSPSYGHTPS-----HHAQFPNHSFKHEDPMGQOG 193
Db 508 VVAFSTQPTPTTGSVLANTL-ATGPAHAPSSSMASHHV----- 548
Qy 194 SLGEQQYSVPPPVYGYCHTPDTSCTGSQALLLRTPYSSD 231
Db 549 -ISQQQHQYPP---GCIEAT--ATSQQVKKRKVYARE 580
```

Search completed: May 10, 2005, 18:45:33
Job time : 40 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 10, 2005, 18:27:44 ; Search time 173 Seconds
(without alignments)
757.759 Million cell updates/sec

Title: US-09-785-019B-335

Perfect score: 1444

Sequence: 1 MQHHHHGSDVRDLNALLP.....TSQLECMWNQMLGATLKG 256

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1386	96.0	249	2 Q6P138	Q6P138 homo sapien
2	1386	96.0	449	1 WTI_HUMAN	P19544 homo sapien
3	1367	94.7	449	1 WTI_PIG	O62651 sus scrofa
4	1340.5	92.8	448	1 WTI_RAT	P49952 rattus norv
5	1329	92.0	449	1 WTI_MOUSE	P22561 mus musculus
6	1094.5	75.8	414	2 Q9I8A1	Q9I8A1 gallus gall
7	1094.5	75.8	417	2 Q9I8A0	Q9I8A0 gallus gall
8	1089.5	75.5	392	2 Q9I030	Q9I030 gallus gall
9	971.5	67.3	407	2 P79958	P79958 xenopus lae
10	957.5	66.3	390	2 O42223	O42223 trachemys s
11	940.5	65.1	409	2 Q9I657	Q9I657 xenopus lae
12	933	64.6	426	2 Q9W611	Q9W611 cynops pyr
13	845.5	58.6	419	2 Q9PU77	Q9PU77 brachydanio
14	822	56.9	417	2 Q90XX6	Q90XX6 oncorhynch
15	776	53.7	386	2 Q90XX8	Q90XX8 oncorhynch
16	769	53.3	250	2 Q98SU4	Q98SU4 brachydanio
17	733	50.8	392	2 Q9IBF0	Q9IBF0 anguilla ja
18	728.5	50.5	388	2 Q90XX7	Q90XX7 oncorhynch
19	715.5	49.5	410	2 Q9JIR9	Q9JIR9 oryzias lat
20	713.5	49.4	418	2 Q90XX4	Q90XX4 oncorhynch
21	707.5	49.0	418	2 Q90XX5	Q90XX5 oncorhynch
22	629	43.6	416	2 O93433	O93433 fugu rubrip
23	525	36.4	288	1 WTI_ALLMI	P50902 alligator m
24	407	28.2	251	2 Q866X3	Q866X3 ovis aries
25	306	21.2	239	1 WTI_SMIMA	P49953 sminchopsis
26	235	16.3	42	2 O18760	O18760 sus scrofa
27	168.5	11.7	431	2 Q9PVG9	Q9PVG9 coturnix co
28	168	11.6	2058	2 Q7PUG9	Q7PUG9 onpheles g
29	166.5	11.5	659	2 Q6C708	Q6C708 yarrowia li
30	161.5	11.2	2716	1 OSA_DROME	Q8IN94 drosophila
31	153.5	10.6	993	2 Q9VY31	Q9VY31 drosophila

Query Match

96.0% Score 1386; DB 2; Length 249;

Best Local Similarity 100.0%; Pred. No. 1.1e-77;

Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

0;

32	153	10.6	812	2	Q8LJ56
33	149.5	10.4	371	2	Q9BH7
34	148.5	10.3	530	2	Q07701
35	147.5	10.2	594	2	Q9VEP4
36	147	10.2	451	2	Q62775
37	146	10.1	548	2	Q6DDW4
38	146	10.1	615	2	Q6EUL5
39	146	10.1	917	2	Q873D8
40	145.5	10.1	576	2	Q9XA04
41	145.5	10.1	906	2	Q6MWG9
42	145	10.0	313	2	Q8L556
43	144.5	10.0	447	2	O73628
44	144.5	10.0	639	2	Q9NVZ9
45	144	10.0	384	2	Q6VFT5

ALIGNMENTS

RESULT 1

ID	Q6P138	PRELIMINARY;	PRT;	249 AA.
AC	Q6P138;			
DT	05-JUL-2004	(Tremblrel. 27, Created)		
DT	05-JUL-2004	(Tremblrel. 27, Last sequence update)		
DT	05-JUL-2004	(Tremblrel. 27, Last annotation update)		
DE	WT1 protein.			
GN	Name=WT1;			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,			
RA	Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,			
RA	Jones S.J., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
RP	[2]			
RC	SEQUENCE FROM N.A.			
RA	Strausberg R.;			
RL	Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC046461; AAH46461.1; -			
DR	GO; GO:0005634; C:nucleus; IEA.			
DR	GO; GO:0003700; F:transcription factor activity; IEA.			
DR	GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.			
DR	InterPro; IPR000976; Wilms_tumour.			
DR	Pfam; PF02165; Wtl; 1.			
DR	PRINTS; PR00049; WILMSTUMOUR.			
SQ	SEQUENCE 249 AA; 25967 MW; 33F53B96A79CBF28 CRC64;			

RL FASEB J. 7:896-903(1993).
RN [14]
RP VARIANT WT1 CYS-366.
RX MEDLINE=92279213; PubMed=1317572;
RA Little M.H., Prosser J., Condie A., Smith P.J., van Heyningen V.,
RA Hastie N.D.;
RT "Zinc finger point mutations within the WT1 gene in Wilms tumor patients.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4791-4795(1992).
RN [15]
RP VARIANTS DDS.
RX MEDLINE=92005721; PubMed=1655284; DOI=10.1016/0092-8674(91)90194-4;
RA Pelletier J., Bruening W., Kashan C.E., Mauer S.M., Manivel J.C.,
RA Striegel J.E., Houghton D.C., Junien C., Habib R., Fouser L.,
RA Fine R.N., Silverman B.L., Haber D.A., Housman D.E.;
RT "Germline mutations in the Wilms' tumor suppressor gene are associated with abnormal urogenital development in Denys-Drash syndrome.";
RL Cell 67:437-447(1991).
RN [16]
RP VARIANTS DDS.
RX MEDLINE=93265053; PubMed=1338906;
RA Baird P.N., Santos A., Groves N., Jadresic L., Cowell J.K.;
RT "Constitutional mutations in the WT1 gene in patients with Denys-Drash syndrome.";
RL Hum. Mol. Genet. 1:301-305(1992).
RN [17]
RP SEQUENCE OF 385-405 FROM N.A., AND VARIANT DDS TRP-394.
RX MEDLINE=93250986; PubMed=1302008;
RA Bruening W., Bardeesy N., Silverman B.L., Cohn R.A., Machin G.A.,
RA Aronson A.J., Housman D., Pelletier J.;
RT "Germline intronic and exonic mutations in the Wilms' tumour gene (WT1) affecting urogenital development.";
RL Nat. Genet. 1:144-148(1992).
RN [18]
RP VARIANTS DDS.
RX MEDLINE=93271983; PubMed=8388765;
RA Little M.H., Williamson K.A., Mannens M., Kelsey A., Gorden C.,
RA Hastie N.D., van Heyningen V.;
RT "Evidence that WT1 mutations in Denys-Drash syndrome patients may act in a dominant-negative fashion.";
RL Hum. Mol. Genet. 2:259-264(1993).
RN [19]
RP VARIANTS DDS TRP-394 AND PRO-398.
RX MEDLINE=94125627; PubMed=8295405;
RA Teuda M., Sakiyama T., Kitagawa T., Watanabe S., Watanabe T.,
RA Takahashi S., Kawaguchi H., Ito K.;
RT "Molecular analysis of two Japanese cases of Denys-Drash syndrome.";
RL J. Inher. Metab. Dis. 16:876-880(1993).
RN [20]
RP VARIANT MESOTHELIOMA GLY-273.
RX MEDLINE=94004972; PubMed=8401592;
RA Park S., Schalling M., Bernard A., Maheswaran S., Shipley G.C.,
RA Roberts D., Fletcher J., Shipman R., Rheinwald J., Demetri G.,
RA Griffin J., Minden M., Housman D.E., Haber D.A.;
RT "The Wilms tumour gene WT1 is expressed in murine mesoderm-derived tissues and mutated in a human mesothelioma.";
RL Nat. Genet. 4:415-420(1993).
RN [21]
RP VARIANT DDS ARG-377.
RX MEDLINE=94156335; PubMed=8112732;
RA Nordenskjold A., Friedman E., Anvret M.;
RT "WT1 mutations in patients with Denys-Drash syndrome: a novel mutation in exon 8 and paternal allele origin.";
RL Hum. Genet. 93:115-120(1994).
RN [22]
RP VARIANT DDS TYR-373.
RX MEDLINE=97114281; PubMed=8956030;
RA Ghahremani M., Chan C.B., Bistrizter T., Aladjem M.M., Tieder M.,
RA Pelletier J.;
RT "A novel mutation H373Y in the Wilms' tumor suppressor gene, WT1, associated with Denys-Drash syndrome.";
RL Hum. Hered. 46:336-338(1996).
RN [23]

RP VARIANTS WT1 SER-181 AND ALA-253.
RX MEDLINE=97268681; PubMed=9108089; DOI=10.1073/pnas.94.8.3972;
RA Schumacher V., Schneider S., Figge A., Wildhardt G., Harms D.,
RA Schmidt D., Weirich A., Ludwig R., Royer-Pokora B.;
RT "Correlation of germ-line mutations and two-hit inactivation of the Query Match 96.0%; Score 1386; DB 1; Length 449;
Best Local Similarity 100.0%; Pred. No. 1.9e-77;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 GSDVRDLNALLPAVPSLGGGGGCGALPVSGAAQWAPVLDFAAPPASAYGSLGGPAPPAPP 68
DB 2 GSDVRDLNALLPAVPSLGGGGGCGALPVSGAAQWAPVLDFAAPPASAYGSLGGPAPPAPP 61
QY 69 PPPPPPHSFIFKQEPGWGGAEPHEEQCLSAFTVHFSQQTGTACACRYGPGPPPPSQAS 128
DB 62 PPPPPPHSFIFKQEPGWGGAEPHEEQCLSAFTVHFSQQTGTACACRYGPGPPPPSQAS 121
QY 129 SGQARMFPNAPYLPSCLESQPAIRNQGYSTVTDGTPSYGHTPSHHAAQFPNHSFKHEDP 188
DB 122 SGQARMFPNAPYLPSCLESQPAIRNQGYSTVTDGTPSYGHTPSHHAAQFPNHSFKHEDP 181
QY 189 MGQGGSLGEGQOYVPPPVYGGCHTPTDCTGSOALLLRTPYSSDNLQYQMTSOLECMTWNQM 248
DB 182 MGQGGSLGEGQOYVPPPVYGGCHTPTDCTGSOALLLRTPYSSDNLQYQMTSOLECMTWNQM 241
QY 249 NLGATLKG 256
DB 242 NLGATLKG 249
RESULT 3
WT1_PIG ID WT1_PIG STANDARD; PRT; 449 AA.
AC O62651;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Wilms' tumor protein homolog.
GN Name=WT1;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 4).
RC STRAIN=LWD; TISSUE=Kidney;
RX MEDLINE=98267201; PubMed=9602131; DOI=10.1016/S0378-1119(98)00112-7;
RA Teurutani N., Oda H., Nakatsuru Y., Imai Y., Zhang S., Ueno Y.,
RA Ishikawa T.;
RT "cDNA cloning and developmental expression of the porcine homologue of WT1.";
RL Gene 211:215-220(1998).
CC -1- FUNCTION: Potential role in transcriptional regulation. Recognizes and binds to the DNA sequence 5'-CGCCCCCGC-3'.
CC -1- SUBUNIT: Interacts with ZNF224 via the zinc-finger region. Interacts with WTAP (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Comment=Experimental confirmation may be lacking for some isoforms;
CC Name=1;
CC IsoId=O62651-1; Sequence=Displayed;
CC Name=2;
CC IsoId=O62651-2; Sequence=VSP_006870, VSP_006871;
CC Name=3;
CC IsoId=O62651-3; Sequence=VSP_006870;
CC Name=4;
CC IsoId=O62651-4; Sequence=VSP_006871;
CC -1- DEVELOPMENTAL STAGE: Expressed during kidney development.
CC -1- SIMILARITY: Belongs to the EGR C2H2-type zinc-finger protein family.

DR	Pfam; PF02165; WT1. 1.	
DR	Pfam; PF00096; zf-C2H2; 4.	
DR	PRINTS; PR00049; WILDMTUMOUR.	
DR	ProDom; PD000003; Znf_C2H2; 2.	
DR	SMART; SM00355; Znf_C2H2; 4.	
DR	PROSITE; PS00028; ZINC_FINGER_C2H2.1; 4.	
DR	PROSITE; PS00157; ZINC_FINGER_C2H2.2; 4.	
KW	Alternative splicing; Anti-oncogene; DNA-binding; Metal-binding;	
KW	Nuclear protein; Repeat; Transcription regulation; Zinc-finger.	
FT	DOMAIN 28 83	
FT	ZN_FING 323 347	
FT	ZN_FING 353 377	
FT	ZN_FING 383 405	
FT	ZN_FING 414 438	
FT	VARSPDIC 250 266	
FT	Missing (in isoform 2 and isoform 3).	
FT	/FTid=VSP_006868.	
FT	Missing (in isoform 2 and isoform 4).	
FT	/FTid=VSP_006869.	
SEQ	SEQUENCE 449 AA; 49246 MW; 962381E5C8D7A380 CRC64;	
Query Match 92.0%; Score 1329; DB 1; Length 449;		
Best Local Similarity 96.8%; Pred. No. 6e-74;		
Matches 241; Conservative 1; Mismatches 5; Indels 2; Gaps 2;		
Qy	9 GSDVRDINALLPAVPSL-GGGGCGALPVSGAAQWAPVLDFAFPACASAYSGSGGPAAPPAP 67	
Db	2 GSDVRDINALLPAVSLGGGGGGCGLPVSGARQWAPVLDFAFPACASAYSLGGGAPPAPA- 60	
Qy	68 PPPPPPPHFFIKQEPSWGGAEPHEEOCLSAFTVHFSGQGTGTAGACRYGFGPPPPPSQA 127	
Db	61 PPPPPPPHFFIKQEPSWGGAEPHEEOCLSAFTLHFSGQGTGTAGACRYGFGPPPPPSQA 120	
Qy	128 SSGQARFNPAPYLPSCLESQPAIRNQGYSTVTFDGTPSYCHTPSHHAAQFPNHSFKHED 187	
Db	121 SSGQARFNPAPYLPSCLESQPIRNQGYSTVTFDGAPSYGHTPSHHAAQFPNHSFKHED 180	
Qy	188 PMGQGSGLGBOQYSVPPPVYGCHTPTDSCGSQLLLRTPYSSDNLVQMTSQLECMTNQ 247	
Db	181 PMGQGSGLGBOQYSVPPPVYGCHTPTDSCGSQLLLRTPYSSDNLVQMTSQLECMTNQ 240	
Qy	248 MNLGATLKG 256	
Db	241 MNLGATLKG 249	
RESULT 6		
Q918A1	PRELIMINARY;	
ID	Q918A1	PRT; 414 AA.
AC	Q918A1	
DT	01-OCT-2000 (TrEMBLrel. 15, Created)	
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)	
DE	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)	
DE	WT1(-KTS) protein.	
GN	Name=WT1(-KTS);	
OS	Gallus gallus (Chicken).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;	
OC	Gallus.	
OX	NCBI_TaxID=9031;	
ON	[1]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=Ovary;	
RA	Kudo T.;	
RL	Submitted (OCT-1999) to the EMBL/GenBank/DBDJ databases.	
DR	EMBL; AB033633; BAA94793.1; -.	
DR	HSP; P08046; I147.	
DR	GO; GO:0005634; C:nucleus; IEA.	
DR	GO; GO:0003676; F:nucleic acid binding; IEA.	
DR	GO; GO:0003700; F:transcription factor activity; IEA.	
DR	GO; GO:0008270; F:zinc ion binding; IEA.	
DR	GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.	
DR	InterPro; IPR000976; Wilmstumour.	
DR	InterPro; IPR007087; Znf_C2H2.	

```
DR Pfam; PF02165; Wt1; 1.
DR Pfam; PF00096; zf-C2H2; 4.
DR PRINTS; PR00049; WILMSTUMOUR.
DR ProDom; PD000003; Znf_C2H2; 2.
DR SMART; SM00355; Znf_C2H2; 4.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 4.
SQ SEQUENCE 414 AA; 46641 MW; 17EB22F8B428A2EF CRC64;

Query Match 75.8%; Score 1094.5; DB 2; Length 414;
Best Local Similarity 81.9%; Pred. No. 1.3e-59;
Matches 203; Conservative 10; Mismatches 18; Indels 17; Gaps 3;

Qy 9 GSDVRDLNALLPAVPSLGGGGGCGGCGGALPVSGAAQWAPVLDFAAPPASAYGSLGGPAPPAPP 68
Db 2 GSDVRDLNALLPSVPSLPNGSNCAAMPVSSAAQWAPVLDFAAPPASAYGSLGGPAPPAPP 50
Qy 69 PPSPPPHSFTIKQPSWGGABPHEEQCLSAFTVHFSQQTGTAGACRYGPGFPAPPAS 128
Db 51 -----PHSFTIKQPSWNGSDPHEEQVLSAFTVHFSQQTGTAGACRYGPGFPAPPAS 104
Qy 129 SGQARMPNAPYLPSCLESQPAIRNQGYSVTVDGTPSYGHTPSHHAAQPNHFSFKHEDP 188
Db 105 SGQARMPNAPYLPSCLESQPAIRNQGYSVTVDGTPSYGHTPSHHAAQPNHFSFKHEDP 164
Qy 189 MGQQSGLGEQQYSVPPVYGGHTPTDCTGSQLLLRTPTYSNDLYQMTSLECMWTNQ 248
Db 165 MSQPSLGDQOYSVPPVYGGHTPTDCTGSQLLLRTPTYSNDLYQMTSLECMWTNQ 224
Qy 249 NLGATLKG 256
Db 225 NLGATLKG 232

RESULT 7
Q918A0 PRELIMINARY; PRT; 417 AA.
AC Q918A0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Wt1(+KTS) protein.
GN Name=Wt1(+KTS);
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RA Kudo T.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB033634; BAA94794.1; -.
DR HSSP; P08046; 1P47.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR00976; Wtms tumour.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF02165; Wt1; 1.
DR Pfam; PF00096; zf-C2H2; 4.
DR ProDom; PD000003; Znf_C2H2; 2.
DR SMART; SM00355; Znf_C2H2; 4.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 4.
SQ SEQUENCE 417 AA; 46957 MW; 47BBF7F6448E7F6C CRC64;

Query Match 75.8%; Score 1094.5; DB 2; Length 417;
Best Local Similarity 81.9%; Pred. No. 1.3e-59;
Matches 203; Conservative 10; Mismatches 18; Indels 17; Gaps 3;

Qy 9 GSDVRDLNALLPAVPSLGGGGGCGGCGGALPVSGAAQWAPVLDFAAPPASAYGSLGGPAPPAPP 68
Db 2 GSDVRDLNALLPSVPSLPNGSNCAAMPVSSAAQWAPVLDFAAPPASAYGSLGGPAPPAPP 50
Qy 69 PPSPPPHSFTIKQPSWGGABPHEEQCLSAFTVHFSQQTGTAGACRYGPGFPAPPAS 128
Db 51 -----PHSFTIKQPSWNGSDPHEEQVLSAFTVHFSQQTGTAGACRYGPGFPAPPAS 104
Qy 129 SGQARMPNAPYLPSCLESQPAIRNQGYSVTVDGTPSYGHTPSHHAAQPNHFSFKHEDP 188
Db 105 SGQARMPNAPYLPSCLESQPAIRNQGYSVTVDGTPSYGHTPSHHAAQPNHFSFKHEDP 164
Qy 189 MGQQSGLGEQQYSVPPVYGGHTPTDCTGSQLLLRTPTYSNDLYQMTSLECMWTNQ 248
Db 165 MSQPSLGDQOYSVPPVYGGHTPTDCTGSQLLLRTPTYSNDLYQMTSLECMWTNQ 224
Qy 249 NLGATLKG 256
Db 225 NLGATLKG 232

RESULT 7
Q918A0 PRELIMINARY; PRT; 417 AA.
AC Q918A0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Wt1(+KTS) protein.
GN Name=Wt1(+KTS);
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RA Kudo T.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB033634; BAA94794.1; -.
DR HSSP; P08046; 1P47.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR00976; Wtms tumour.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF02165; Wt1; 1.
DR Pfam; PF00096; zf-C2H2; 4.
DR ProDom; PD000003; Znf_C2H2; 2.
DR SMART; SM00355; Znf_C2H2; 4.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 4.
SQ SEQUENCE 417 AA; 46957 MW; 47BBF7F6448E7F6C CRC64;

Query Match 75.8%; Score 1094.5; DB 2; Length 417;
Best Local Similarity 81.9%; Pred. No. 1.3e-59;
Matches 203; Conservative 10; Mismatches 18; Indels 17; Gaps 3;

Qy 9 GSDVRDLNALLPAVPSLGGGGGCGGCGGALPVSGAAQWAPVLDFAAPPASAYGSLGGPAPPAPP 68
Db 2 GSDVRDLNALLPSVPSLPNGSNCAAMPVSSAAQWAPVLDFAAPPASAYGSLGGPAPPAPP 50
Qy 69 PPSPPPHSFTIKQPSWGGABPHEEQCLSAFTVHFSQQTGTAGACRYGPGFPAPPAS 128
Db 51 -----PHSFTIKQPSWNGSDPHEEQVLSAFTVHFSQQTGTAGACRYGPGFPAPPAS 104
Qy 129 SGQARMPNAPYLPSCLESQPAIRNQGYSVTVDGTPSYGHTPSHHAAQPNHFSFKHEDP 188
Db 105 SGQARMPNAPYLPSCLESQPAIRNQGYSVTVDGTPSYGHTPSHHAAQPNHFSFKHEDP 164
Qy 189 MGQQSGLGEQQYSVPPVYGGHTPTDCTGSQLLLRTPTYSNDLYQMTSLECMWTNQ 248
Db 165 MSQPSLGDQOYSVPPVYGGHTPTDCTGSQLLLRTPTYSNDLYQMTSLECMWTNQ 224
Qy 249 NLGATLKG 256
Db 225 NLGATLKG 232

RESULT 8
Q91030 PRELIMINARY; PRT; 392 AA.
AC Q91030;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Chick Wilm's tumour protein (fragment).
GN Name=CWT1;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole embryo;
RA Kent J., Coriat A.M., Sharpe P.T., Hastie N., van Heyningen V.;
RL "The evolution of Wt1 sequence and expression in the vertebrates.";
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole embryo;
RA Kent G.R.L.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; X85731; CAA59736.1; -.
DR HSSP; Q60980; 1P7A.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:006355; P:regulation of transcription, DNA-dependent; IEA.
DR Pfam; PF02165; Wt1; 1.
DR Pfam; PF00096; zf-C2H2; 3.
DR PRINTS; PR00049; WILMSTUMOUR.
DR ProDom; PD000003; Znf_C2H2; 2.
DR SMART; SM00355; Znf_C2H2; 3.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 3.
FT NON TER 392
SQ SEQUENCE 392 AA; 43869 MW; 761F01D350E4EDBF CRC64;

Query Match 75.8%; Score 1089.5; DB 2; Length 392;
Best Local Similarity 81.5%; Pred. No. 2.5e-59;
Matches 202; Conservative 11; Mismatches 18; Indels 17; Gaps 3;

Qy 9 GSDVRDLNALLPAVPSLGGGGGCGGCGGALPVSGAAQWAPVLDFAAPPASAYGSLGGPAPPAPP 68
Db 2 GSDVRDLNALLPSVPSLPNGSNCAAMPVSSAAQWAPVLDFAAPPASAYGSLGGPAPPAPP 50
```



```

ID Q91657 PRELIMINARY; PRT; 409 AA.
AC Q91657;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE WT1.
GN Name=WT1;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96363858; PubMed=8725280;
RX DOI=10.1002/(SICI)1097-0177(199606)206:2<131::AID-AJA2>3.3.CO;2-I;
RA Carroll T.J., Vize P.D.;
RT "Wilms' tumor suppressor gene is involved in the development of
RT disparate kidney forms: evidence from expression in the Xenopus
RT pronephros.";
RL Dev. Dyn. 206:131-138(1996).
DR EMBL; U42011; AB53152.1; -.
DR HSP; P08046; IP47.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR Pfam; PF02165; Wt1, 1.
DR Pfam; PF00096; zf-C2H2; 4.
DR PRINTS; PR00049; WILMTUMOUR.
DR ProDom; PD000003; Znf_C2H2; 2.
DR SMART; SM00355; Znf_C2H2; 4.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 4.
SQ SEQUENCE 409 AA; 46186 MW; 2217FC04612CDE10 CRC64;

Query Match 65.1%; Score 940.5; DB 2; Length 409;
Best Local Similarity 71.7%; Pred. No. 3.6e-50;
Matches 177; Conservative 19; Mismatches 30; Indels 21; Gaps 5;

QY 9 GSDVRDLNALLPAVPSLGGGGGCGALPVSGAAQWAPVLDFAAPPASAYGSLGGPAPPAPP 68
DB 2 GSDVRDMN-LLPVPSSLSGNSCNMPVSSAAQWAPVLDFA-PRG----- 42
QY 69 PPPPPPHSFHKQEPSWGGGAEPHEEQCLSAFTVHFSQFTGTAGACRYGFGPPPPSQAS 128
DB 43 PLQLPDSLFIKQEPW-NPDPHEDQCLSAFTVHFSQFTGTAGACRYGFGAPTPSQAT 101
QY 129 SGQARMFNPAPYLPSCLESQPAIRNQGYSVTFTDGTPTSGHSHAAQFPNHSFKHEDP 188
DB 102 TQGARMFNPAPYLSNCLDNQGMENQGYSAVAFDGTPTSGHTPS-HTSQFTNHSFKHEDP 160
QY 189 MQQGSGLGEQOQSVPPPVYGGHTPTDCTGSQLLLRTPYSSDNLQYMTSQLECMWNQM 248
DB 161 LSQQTSLGEQOQSVPPPVYGGHTPTDCTGSQLLLRTPYSSDNLQYMTSQLECMWNQM 220
QY 249 NLGATLK 255
DB 221 NLGSSLK 227

RESULT 12
Q9W611 PRELIMINARY; PRT; 426 AA.
ID Q9W611
AC Q9W611;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE WT1.
OS Cynops pyrrhogaster (Japanese common newt).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Cynops.

```

```

OX NCBI_TaxID=8330;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99081568; PubMed=9865970;
RX Nakayama Y., Yamamoto T., Matsuda Y., Abe S.-I.;
RT "Cloning of cDNA for newt Wt1 and the differential expression during
RT spermatogenesis of the Japanese newt, Cynops pyrrhogaster.";
RL Dev. Growth Differ. 40:599-608(1998).
DR EMBL; AB013888; BAA76399.1; -.
DR HSP; P08046; IP47.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000976; Wilms tumour.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF02165; Wt1, 1.
DR Pfam; PF00096; zf-C2H2; 4.
DR PRINTS; PR00049; WILMTUMOUR.
DR ProDom; PD000003; Znf_C2H2; 2.
DR SMART; SM00355; Znf_C2H2; 4.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 4.
SQ SEQUENCE 426 AA; 47590 MW; 46A0B150A9F79C6C CRC64;

Query Match 64.6%; Score 933; DB 2; Length 426;
Best Local Similarity 67.5%; Pred. No. 1.1e-49;
Matches 172; Conservative 22; Mismatches 37; Indels 24; Gaps 4;

QY 9 GSDVRDLNALLPAVPSLGGGGGCGALPVSGAAQWAPVLDFAAPPASAYGSLGGPAPPAPP 68
DB 2 GSDVRDMNALLPPVSSLSGSGSCIPMGGSQWAPMLDFSP--GAPYGSLSA----- 50
QY 69 PPPPPPHSFHKQEPSWGGGAEPHEEQCLSAFTVHFSQFTGTAGACRYGFGPPPP--- 123
DB 51 -----PHSYIKQEPSWGGGSLHEDQCLSAKVTVHFSQITGTAEACRYGAFGAPSSRA 104
QY 124 --PSQASSGQARMFPNAPYLPSCLESQPAIRNQGYSVTFTDGTPTSGHSHAAQFPNH 181
DB 105 PQSQPQAQVRMFSNGPYLPNCLENPQAIRNQGYNALAFDGAAPSYGHTPSHVAQFTNH 164
QY 182 SFKHEDPMQGGSLGBOQSVPPPVYGGHTPTDCTGSQLLLRTPYSSDNLQYMTSQLE 241
DB 165 SFKHEDPMQSQTSLAQOQSVPPPVYGGHTPTDCTGSQLLLRTPYSSDNLQYMTSQLE 224
QY 242 CMTWNQNLGATLK 256
DB 225 CMTWNQNLGSSPKG 239

RESULT 13
Q9PUT7 PRELIMINARY; PRT; 419 AA.
ID Q9PUT7
AC Q9PUT7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Wilms' tumor suppressor.
GN Name=wt1;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Smith S.I., Down M., Power M., Boyd A.W.;
RA Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF144550; AAF00123.1; -.
DR HSP; P08046; IP47.
DR ZFIN; ZDB-GENE-980526-558; wt1.

```

DR GO:0005634; C:nucleus; IEA.
DR GO:0003676; F:nucleic acid binding; IEA.
DR GO:0003700; F:transcription factor activity; IEA.
DR GO:0008270; F:zinc ion binding; IEA.
DR GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000976; Wilms tumour.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF02165; WT1; 1.
DR Pfam; PF00096; zf-C2H2; 4.
DR PRINTS; PR00049; WILMSTUMOUR.
DR ProDom; PD000003; Znf_C2H2; 2.
DR SMART; SM00355; Znf_C2H2; 4.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 4.
SQ SEQUENCE 419 AA; 46925 MW; 606ADFEDA619EECD CRC64;

Query Match 58.6%; Score 845.5; DB 2; Length 419;
Best Local Similarity 65.5%; Pred. No. 2.4e-44;
Matches 167; Conservative 17; Mismatches 42; Indels 29; Gaps 9;

Qy 9 GSDVRLNALLPAVPSL-GGGGGCALPVSGAAQWAPVLDLDF---APPGASAYGSLGGPAPP 64
|||||
Db 2 GSDVRLNALLPPVPLPGGNGCTLPVSSTPQPPMLDFHTGAP-----YGSLLA----- 51
|||||
Qy 65 PAPPPPPPPHSFIKQEPSWGGAEPEHE-OC-LSAFTVHPSGQFTGTAGACRYGPGPP 122
|||||
Db 52 -----QHSPFKQEPSWGGTADPHEDPHCGLSAFTVHPSGQFTGT-GACRYGAFGAP 100
|||||
Qy 123 PPSQASSGOARMFPNAPVLPSCLESQPAIRNOGYSTVTFDGTPTSGYGHTPSHHAAQFPNH 182
|||||
Db 101 AASQPPSPQRMFNSPFLSCMDSQSSRNQGGVGTVAFDGASNYGHTPSHHTQFPNH 160
|||||
Qy 183 FKHEDPMGQGGSLGEQQYVPPVYGGHTPTDSCGQALLLRTPY-SSDNLYQMTSQL 241
|||||
Db 161 FKHEDSITQSNMGDQYVPPVYGGHTPTDSCGQALLLRPNYSSDNLYQMASQLE 220
|||||
Qy 242 CMTWNQMN-LGATLK 255
|||||
Db 221 CMGNPNVNSTASTIK 235
|||||

RESULT 14
Q90XX6 ID Q90XX6 PRELIMINARY; PRT; 417 AA.
AC Q90XX6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Wilms' tumor suppressor lb variant.
GN Name=WT-tlb;
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21337607; PubMed=11444705; DOI=10.1139/gen-44-3-455;
RA Brunelli J.P., Robison B.D., Thorgaard G.H.;
RT "Ancient and recent duplications of the rainbow trout Wilms' tumor gene."
RL Genome 44:455-462(2001).
DR EMBL; AF334672; AAK52721.1; -.
DR HSSP; P08046; 1P47.
DR GO:0005634; C:nucleus; IEA.
DR GO:0003676; F:nucleic acid binding; IEA.
DR GO:0003700; F:transcription factor activity; IEA.
DR GO:0008270; F:zinc ion binding; IEA.
DR GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR Pfam; PF02165; WT1; 1.
DR Pfam; PF00096; zf-C2H2; 4.
DR PRINTS; PR00049; WILMSTUMOUR.
DR ProDom; PD000003; Znf_C2H2; 2.
DR SMART; SM00355; Znf_C2H2; 4.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 4.
SQ SEQUENCE 386 AA; 43286 MW; 05622EF7642FC9E5 CRC64;

Query Match 53.7%; Score 776; DB 2; Length 386;
Best Local Similarity 66.8%; Pred. No. 4.1e-40;
Matches 151; Conservative 15; Mismatches 36; Indels 24; Gaps 8;

Qy 9 GSDVRLNALLPAVPSL-GGGGGCALPVSGAAQWAPVLDLDFAPPGASAYGSLGGPAPPAP 67
|||||

DR SMART; SM00355; Znf_C2H2; 4.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 4.
SQ SEQUENCE 417 AA; 46557 MW; 5217620CD471D030 CRC64;

Query Match 56.9%; Score 822; DB 2; Length 417;
Best Local Similarity 64.5%; Pred. No. 6.7e-43;
Matches 165; Conservative 22; Mismatches 37; Indels 32; Gaps 11;

Qy 9 GSDVRLNALLPAVPSL-GGGGGCALPVSGAAQWAPVLDLDF---APPGASAYGSLGGPAPP 64
|||||
Db 2 GSDVRLNALLPPVPLPGGNGCTLPVSSAPQWGPVLDFTHTGAP-----YSSLLA----- 51
|||||
Qy 65 PAPPPPPPPHSFIKQEPSWGGAEPEHE-OC-LSAFTVHPSGQFTGTAGACRYGPGP-P 121
|||||
Db 52 -----PHSFIKQEPSWSSGDPOEDPHCGLSAFTLHPSGQFTGT-GACRYGAFGAP 100
|||||
Qy 122 PPSQASSGOARMFPNAPVLPSCLESQPAIRNOGYSTVTFDGTPTSGYGHTPSHHAAQFPNH 181
|||||
Db 101 PPSQPPSPQRMFNSPFLSCMDSQSSRNQGY--AFDGATNYGHTPTSHHSSQFLSH 158
|||||
Qy 182 SFKHEDPMGQGGSLGEQQYVPPVYGGHTPTDSCGQALLLRTPY-SSDNLYQMTSQL 240
|||||
Db 159 SFKDENSQAQTSWGEQYVPPVYGGHTPTDSCGQALLLRPNYSSDNLYQMASQL 218
|||||
Qy 241 ECMTWNQMN-LGATLK 255
|||||
Db 219 ECMAWNPNVNSTASTIK 234
|||||

RESULT 15
Q90XX8 ID Q90XX8 PRELIMINARY; PRT; 386 AA.
AC Q90XX8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Wilms' tumor suppressor 1a.
GN Name=WT-t1a;
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21337607; PubMed=11444705; DOI=10.1139/gen-44-3-455;
RA Brunelli J.P., Robison B.D., Thorgaard G.H.;
RT "Ancient and recent duplications of the rainbow trout Wilms' tumor gene."
RL Genome 44:455-462(2001).
DR EMBL; AF334670; AAK52719.1; -.
DR HSSP; P08046; 1P47.
DR GO:0005634; C:nucleus; IEA.
DR GO:0003676; F:nucleic acid binding; IEA.
DR GO:0003700; F:transcription factor activity; IEA.
DR GO:0008270; F:zinc ion binding; IEA.
DR GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR Pfam; PF02165; WT1; 1.
DR Pfam; PF00096; zf-C2H2; 4.
DR PRINTS; PR00049; WILMSTUMOUR.
DR ProDom; PD000003; Znf_C2H2; 3.
DR SMART; SM00355; Znf_C2H2; 4.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 4.
SQ SEQUENCE 386 AA; 43286 MW; 05622EF7642FC9E5 CRC64;

Query Match 53.7%; Score 776; DB 2; Length 386;
Best Local Similarity 66.8%; Pred. No. 4.1e-40;
Matches 151; Conservative 15; Mismatches 36; Indels 24; Gaps 8;

Qy 9 GSDVRLNALLPAVPSL-GGGGGCALPVSGAAQWAPVLDLDFAPPGASAYGSLGGPAPPAP 67
|||||

```
Db      2  GSDVRDLNALLPVPSLSGNGNCTLPVSSAPQWGPVLDFT--GTPYSSLA----- 51
QY      68  PPPPPPPHSHFIKQEPSSWGAEPHE-QC-LSAFTVHESGQFTGTAGACRYGPG-PPPP 124
Db      52  -----PHFFIKQEPSSWGGDPHEDPHCGLSAFTVHESGQFTGT-GACRYGAGGAPPPP 103
QY     125  SQASSQARMFPNAPYLPSCLSQPAIRNQYSTVTFTDGTSPSYGHTPSSHAAQFFNHSFK 184
Db     104  SQPPPSQPRMFSNAPVLTNCMDTQPPSRNQYS--AFDGTNYGHTPTHSSQFFNHSFK 161
QY     185  HEDPMQOQSLGHEQOQYSVPPVYVYCHTPTDCTGSOALLLRTPYSS 230
Db     162  HEDSLAQOTSMGEQOQYVPPVYVYCHTPTSDSCAGSOALLLRNPYNS 207
```

Search completed: May 10, 2005, 18:44:48
Job time : 175 secs